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OM protein - protein search, using sw model

Run on: October 28, 2005, 17:47:28 ; Search time 43 Seconds
(without alignments)
484.351 Million cell updates/sec

Title: US-09-769-744D-26
Perfect score: 1387
Sequence: 1 MGIALENNVFTYQEGTPLAS.....GVSRKRLPIKIEEPKESLNG 279

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1386	99.9	279	4	US-09-583-110-4380
2	1386	99.9	280	4	US-09-107-433-4838
3	844.5	60.9	316	4	US-09-134-000C-4732
4	836.5	60.3	284	4	US-09-107-532A-6030
5	608	43.8	288	3	US-09-134-001C-3292
6	543	39.1	180	4	US-09-214-307A-2
7	508	36.6	300	4	US-09-861-451A-42
8	468.5	33.8	285	4	US-09-107-532A-6376
9	435.5	31.4	272	4	US-09-134-000C-4733
10	412.5	29.7	261	4	US-09-583-110-4382
11	402	29.0	290	3	US-09-134-001C-3273
12	396.5	28.6	249	4	US-09-107-433-4031
13	381.5	27.5	350	4	US-09-107-532A-6978
14	378.5	27.3	357	4	US-09-134-000C-4963
15	373	26.9	361	4	US-09-107-532A-6490
16	371	26.7	264	4	US-09-134-000C-6301
17	368	26.5	247	4	US-09-134-000C-4300
18	366.5	26.4	281	4	US-09-489-039A-10009
19	357	25.7	272	4	US-09-861-451A-4
20	356	25.7	247	4	US-09-107-532A-4327
21	354.5	25.6	353	4	US-09-583-110-4827
22	352	25.4	286	4	US-09-540-236-2931
23	351	25.3	265	4	US-09-710-279-2500
24	348	25.1	246	4	US-09-583-110-4713
25	348	25.1	255	4	US-09-107-433-3563
26	348	25.1	402	4	US-09-107-532A-5360
27	347.5	25.1	246	4	US-09-489-039A-13116

28	346	24.9	242	4	US-09-583-110-2985	Sequence 2985, Ap
29	346	24.9	245	4	US-09-107-433-4827	Sequence 4827, Ap
30	345.5	24.9	254	4	US-09-902-540-16627	Sequence 16627, A
31	345	24.9	242	3	US-09-134-001C-3832	Sequence 3832, Ap
32	344.5	24.8	227	4	US-09-634-238-289	Sequence 289, App
33	344	24.8	369	4	US-09-328-352-6905	Sequence 6905, Ap
34	343	24.7	244	4	US-09-583-110-2710	Sequence 2710, Ap
35	342	24.7	244	3	US-08-919-573-2	Sequence 2, Appl1
36	342	24.5	244	3	US-08-919-573-4	Sequence 4, Appl1
37	340.5	24.5	198	4	US-10-162-012-36	Sequence 36, Appl
38	339	24.4	317	4	US-09-134-000C-5339	Sequence 5339, Ap
39	338.5	24.4	248	3	US-09-134-001C-3731	Sequence 3731, Ap
40	337	24.3	357	3	US-09-134-001C-4891	Sequence 4891, Ap
41	334.5	24.1	265	4	US-09-489-039A-12065	Sequence 12065, A
42	332.5	24.0	258	4	US-09-328-352-4625	Sequence 4625, Ap
43	331	23.9	252	4	US-09-583-110-5309	Sequence 5309, Ap
44	331	23.9	360	4	US-09-543-681A-6466	Sequence 6466, Ap
45	330	23.8	319	4	US-09-489-039A-8116	Sequence 8116, Ap

ALIGNMENTS

RESULT 1

US-09-583-110-4380
; Sequence 4380, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus.
; FILE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4380
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4380

Query Match 99.9%; Score 1386; DB 4; Length 279;
Best Local Similarity 99.6%; Pred. No. 5e-143;
Matches 278; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGIALENNVFTYQEGTPLASALSDVSLTIEDGSGYALIGHTGSGKSTLIQLLGLLVP	60
DB	1	MGIALENNVFTYQEGTPLASALSDVSLTIEDGSGYALIGHTGSGKSTLIQLLGLLVP	60
QY	61	QGSVRVFDLTITSTSKNKDIQIRKQVGLVFPFAENQIFETVLKDVAFQFQNGVSEED	120
DB	61	QGSVRVFDLTITSTSKNKDIQIRKQVGLVFPFAENQIFETVLKDVAFQFQNGVSEED	120
QY	121	AVKTAREKALVGDIDSLFDRSPFELSGGQRRVAIAGILAMPAILVLDDEPTAGLDPLG	180
DB	121	AVKTAREKALVGDIDSLFDRSPFELSGGQRRVAIAGILAMPAILVLDDEPTAGLDPLG	180
QY	181	RKELMTLTKLHOSGMTIVLVTLMDDVAEYANQVYVMEKGRLVKGGKPSDVFQDVVFWME	240
DB	181	RKELMTLTKLHOSGMTIVLVTLMDDVAEYANQVYVMEKGRLVKGGKPSDVFQDVVFWME	240
QY	241	EVOLGVPKITAFCKRLADRGVSFKRLPIKIEEPKESLNG	279
DB	241	EVOLGVPKITAFCKRLADRGVSFKRLPIKIEEPKESLNG	279

RESULT 2


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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085, 598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6030:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 284 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...284
; SEQUENCE DESCRIPTION: SEQ ID NO: 6030:
US-09-107-532A-6030

Query Match 60.3%; Score 836.5; DB 4; Length 284;
Best Local Similarity 59.2%; Pred. No. 6.1e-83;
Matches 161; Conservative 50; Mismatches 60; Indels 1; Gaps 1;

QY 1 MGIALENVFTYQEGTPLASALSVDLSLTIEDGSYTALIGHTSGKSTLQLLGLLVPS 60
DB 12 MDIRPEQVDFTYQNTPEQRALEFDINMTIKENSYALVGHGTSGKSTLQLHLNALVKPT 71

QY 61 QGSVRVFDLTITSTSKNDIRQKQVGLVFOFAENQIFETVLKDVAFGPQNFVSEED 120
DB 72 SGTVHIGERDIQPDNTKMLKPKRKVGIVFQPEAQLFEETVAKDIAGPKNFGVSEEE 131

QY 121 AVKTAREKALVGDIESLDRSPFELSGGQMRRAIAGILAMEPAIILVLDDEPTAGLDPLG 180
DB 132 ALVLAKETLEQGLDESILERSPFELSGGQMRRAIAGILAMEPAIILVLDDEPTAGLDPOG 191

QY 181 RKELMTLTKLH-QSGMTIVLTHLMDVVAEYANQVYMEKRLVKGKPSDVFDVFM 239
DB 192 RKEMEMFWRLHKEQITIVLTHLMDVVAEYANQVYMEKRLVKGKPSDVFDVFM 251

QY 240 BEVQLGVPKITAFCKRLADR-GVSFKRLPIKIEP 271
DB 252 KEKQLGVPITATEPAELMANGMNFATLPLTAE 283

RESULT 5
US-09-134-001C-3292
; Sequence 3292, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134, 001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3292
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3292
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Query Match 43.8%; Score 608; DB 3; Length 288;
Best Local Similarity 43.3%; Pred. No. 6e-58;
Matches 119; Conservative 65; Mismatches 89; Indels 2; Gaps 2;

QY 1 MGIALENVFTYQEGTPLASALSVDLSLTIEDGSYTALIGHTSGKSTLQLLGLLVPS 60
DB 3 MSIQPNQVSYIQGTTPYEFAIKNVSLTLEQKYAIIGTSGKSTLQHLNALVKPT 62

QY 61 QGSVRVFDLTITSTSKNDIRQKQVGLVFOFAENQIFETVLKDVAFGPQNFVSEED 120
DB 63 TGSVNINGLEVNTKDKHLRHRKEVGVPFQPSQLFEDSVEKEIEFGPKNFNNLKN 122

QY 121 AVKTAREKALVGDIESLDRSPFELSGGQMRRAIAGILAMEPAIILVLDDEPTAGLDPLG 180
DB 123 VKDAFQQLLELGFSPRNVMSSPFFQMSGQMRKIAIVSLAMDPOVILDEPTAGLDPS 182

QY 181 RKELMTLTKLH-QSGMTIVLTHLMDVVAEYANQVYMEKRLVKGKPSDVFDVFM 239
DB 183 KHQVMSLIKIQIEENKTIILVSHDMDVARYSDEVVMNKGITVEKSNRNLFNQKTQL 242

QY 240 BEVQLGVPKITAFCKRLADR-GVSFKRLPIKIEP 273
DB 243 LKWHIELPKVVKLQDKIEKKYNMPLPKLATNEEF 277
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RESULT 6
US-09-214-307A-2
; Sequence 2, Application US/09214307A
; Patent No. 6544516
; GENERAL INFORMATION:
; APPLICANT: NEUTEC PHARMA PLC
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF INFECTIONS OF GRAM POSITIVE
; TITLE OF INVENTION: COCCI
; FILE REFERENCE: PM 259204
; CURRENT APPLICATION NUMBER: US/09/214,307A
; CURRENT FILING DATE: 1999-01-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01830
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: GB9614274.0
; PRIOR FILING DATE: 1996-07-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-09-214-307A-2
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Query Match 39.1%; Score 543; DB 4; Length 180;
Best Local Similarity 62.4%; Pred. No. 3.6e-51;
Matches 106; Conservative 26; Mismatches 38; Indels 0; Gaps 0;

QY 7 NVNFTYQEGTPLASALSVDLSLTIEDGSYTALIGHTSGKSTLQLLGLLVPSQSVRV 66
DB 11 NSRFTYQNTPEQRALEFDINMTIKENSYALVGHGTSGKSTLQLHLNALVKPTSGTVHI 70

QY 67 FDTLITSTSKNDIRQKQVGLVFOFAENQIFETVLKDVAFGPQNFVSEEDAVKTAR 126
DB 71 GERDIQPDNTKMLKPKRKVGIVFQPEAQLFEETVAKDIAGPKNFGVSEELVLAK 130

QY 127 EKLALVGDIESLDRSPFELSGGQMRRAIAGILAMEPAIILVLDDEPTAGL 176
DB 131 ETLEQVGLDESILERSPFELSGGQMRRAIAGILAMEPAIILVLDDEPTAGL 180
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RESULT 7
US-09-861-451A-42
; Sequence 42, Application US/09861451A
; Patent No. 6759516
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific & Industrial Research Orga
; TITLE OF INVENTION: Methods of Identifying Antigen Gene Sequences
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; FILE REFERENCE: FF34033/01
; CURRENT APPLICATION NUMBER: US/09/861,451A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PP7273
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Deduced protein
; OTHER INFORMATION: sequence from clone PAD913
US-09-861-451A-42

Query Match          36.6%; Score 508; DB 4; Length 300;
Best Local Similarity 37.5%; Pred. No. 5.5e-47;
Matches 111; Conservative 49; Mismatches 90; Indels 46; Gaps 4;

QY 1 MGIALENVFTYQEGTPLASAAALSDVSLTIEDGSYTALIGHTSGKSTILQLLGLLVP 60
Db 1 MKIKAKITVKIYDQKLPSELKALDKVTTTEINQGEFIALIGQTGSGKTTFIQHMAALLPD 60
QY 61 QGSVR--VFDTLTSTSKND-----IRQIRKOVGLVFOFAENQIFEE 101
Db 61 QGEIYLYFD-----SKNQEKLVVQKPRFRKKLKFINEIRRVGVVFOFAEYQLFEQ 114
QY 102 TVLKDVAFQPNQFVSEBDVKTAREKLAALVIGIDSLDFDRSPFELSGGQMRVAIAGILA 161
Db 115 TIEKDIIFGAVSMGTPKNEAKKIAAEIITELVGLDQSFLOKSPFELSGGQKRRVAIAGILA 174
QY 162 MEPAILVLDEPTAGLDIPGRKELMTLFLKKLHQSMTIVLVTHLMDVDAEYANOVVVMKG 221
Db 175 MDPDIIFDEPTAGLDIPQGLKMLILDITLYKKGKTIILATHDLDSVLEWTKRCIFFKDG 234
QY 222 RLKVGKPSDVFDVVEEVQLGVPKITAFCKRLADRGVSFKRLPIKIESFKESL 277
Db 235 RIYDGDYTSILANNKFL-----IENKMLPTNLLNFKRL 269

RESULT 8
US-09-107-532A-6376
; Sequence 6376, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
```

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; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6376:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...285
; SEQUENCE DESCRIPTION: SEQ ID NO: 6376:
US-09-107-532A-6376

Query Match          33.8%; Score 468.5; DB 4; Length 285;
Best Local Similarity 40.7%; Pred. No. 1e-42;
Matches 107; Conservative 53; Mismatches 88; Indels 15; Gaps 6;

QY 3 IALENVFTYQEGTPLASAAALSDVSLTIEDGSYTALIGHTSGKSTILQLLGLLVP 62
Db 11 IELEKINYKQPD--LRPALKDVFTIDKGEWIAIIGHNGSGKSTLAKTINGLLLP 68
QY 63 SVRVFDLTITSTSKNKDQIRKQVGLVFOFAENQIFETVLKDVAFQPNQFVSEED-- 120
Db 69 IVKVGNGQIL---DEENITWIRQVGMVFNQPNQFVGVSTVEDDVAFLGNQGI 124
QY 121 -AVKTAREKLAALVIGIDSLDFDRSPFELSGGQMRVAIAGILAMEPAILVLDEPTAGLD 179
Db 125 VRVKDALEKVRMA---EFASREPARLSGGQKQKRVAGVVALRPDIILDEATSM 180
QY 180 GRKELMTLFFKKL-HQSGMTIVLVTHLMDVDAEYANOVVMEKGRLVKGGKPSDVFD 238
Db 181 GREVISTIKIKESQLTVISITHDIDEAAN-ANRILVMRQGLVREGTPEIF 239
QY 239 MEEVQLGVPKITAFCKRLADRGV 261
Db 240 LIDLGLDLPPEPKLSALKERG 262

RESULT 9
US-09-134-000C-4733
; Sequence 4733, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4733
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4733

Query Match          31.4%; Score 435.5; DB 4; Length 272;
Best Local Similarity 39.3%; Pred. No. 3.9e-39;
Matches 96; Conservative 53; Mismatches 88; Indels 7; Gaps 4;

QY 19 ASAAALSDVSLTIEDGSYTALIGHTSGKSTILQLLGLLVP 78
Db 12 ASPALKDVFSIQGEWVAIIGHNGSGKSTLAKTINGLLLPAACTIKVGGKELNEA----- 67
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; INFORMATION FOR SEQ ID NO: 4031:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 249 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: YES
;   ORIGINAL SOURCE:
;     ORGANISM: Streptococcus pneumoniae
;   FEATURE:
;     NAME/KEY: misc feature
;     LOCATION: (B) LOCATION 1...249
;     SEQUENCE DESCRIPTION: SEQ ID NO: 4031:
US-09-107-433-4031

Query Match      28.6%; Score 396.5; DB 4; Length 249;
Best Local Similarity 37.1%; Pred. No. 6.3e-35;
Matches 86; Conservative 59; Mismatches 78; Indels 9; Gaps 5;

QY 3 IALENNVTYQEGTPLASAAALSDVSLTIEDGSGYALIGHTGSGKSTILQLLGLLVPSQG 62
DB 11 IDVKNLSFRYKQNYID--VKDITFHVKRGEWLSIVGHGSGKSTTVRLIDGLLEASG 68
QY 63 SVRVFDTLITSTSKNKDIRKQVGLVFPQAEQIPEETVLKDVAFQPGQFVSEDAV 122
DB 69 EIVDQGRLT-----BENWNIRKQIGMVFQPDNFQVGTATVEDDVAFLGQGLSRQENK 124
QY 123 KTAREKALVGDIDSLFDRSPFELSGGQMRVVAIGAILAMEPAIILVDEPTAGLDPLGRK 182
DB 125 KRVEBALVGLMD--FKKREPARLSGGQKQKQVAGVVALRPAIILDEATSMLDPEGR 183
QY 183 ELMTLFFKKLHQS-GMTIVLVTHLMDDDVAEYANQVVMKGRVLVKGKPSDVF 233
DB 184 ELIGTVKGIKDYDMTVISITHDLSEIA-MSDRLVLVRKREIESTSPRELFP 234

RESULT 13
US-09-107-532A-6978
; Sequence 6978, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6978:
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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 350 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: YES
;   ORIGINAL SOURCE:
;     ORGANISM: Enterococcus faecium
;   FEATURE:
;     NAME/KEY: misc feature
;     LOCATION: (B) LOCATION 1...350
;     SEQUENCE DESCRIPTION: SEQ ID NO: 6978:
US-09-107-532A-6978

Query Match      27.5%; Score 381.5; DB 4; Length 350;
Best Local Similarity 40.7%; Pred. No. 4.7e-33;
Matches 96; Conservative 48; Mismatches 81; Indels 11; Gaps 6;

QY 3 IALENNVTYQEGTPLASAAALSDVSLTIEDGSGYALIGHTGSGKSTILQLLGLLVPSQG 62
DB 10 IQLTNVKKTF-NGKNGNIQAVNDVSLNVEKGDYIGVYGAGKSTLVRLNLGLLELPTSG 68
QY 63 SVRVFDTLITSTSKNKDIRKQVGLVFPQAEQIPEETVLKDVAFQPGQFVSEDAV 122
DB 69 EIVNDQDITKL--KNKSLRTFRKKGIMFQHF-NLLWSRTVLENIQLPLELAGVPKSKRK 126
QY 123 KTAREKALVGDIDSLFDRSPFELSGGQMRVVAIGAILAMEPAIILVDEPTAGLDPLGRK 182
DB 127 ERABELLRLVGL-SGRGQAVPSQLSGGQKQKQVAGIARALANDPEILLCDEATSDLPQTE 185
QY 183 ELMTLFF---KKLHQSGMTIVLVTHLMDDDVAEYANQVVMKGRVLVKGKPSDVFQ 234
DB 186 EVDLLLAINKKLN---LTIIVLITHMNVRKKNKVAVMELGKVGVEGDVLTVFR 238

RESULT 14
US-09-134-000C-4963
; Sequence 4963, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4963
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4963

Query Match      27.3%; Score 378.5; DB 4; Length 357;
Best Local Similarity 39.2%; Pred. No. 1e-32;
Matches 91; Conservative 52; Mismatches 84; Indels 5; Gaps 5;

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DB 3 IELKNISVTFQO--KKQEIQAQVDVSLTIDKGDYIGVYGAGKSTLVRLINLLQRPQTAG 61
QY 63 SVRVFDTLITSTSKNKDIRKQVGLVFPQAEQIPEETVLKDVAFQPGQFVSEDAV 122
DB 62 TVIINKENILTFSK--KELRQQRKKIGMIFQHF-NLMKERTIFSNIIDPSLKYSLGSKSRR 119
QY 123 KTAREKALVGDIDSLFDRSPFELSGGQMRVVAIGAILAMEPAIILVDEPTAGLDPLGRK 182
DB 120 QKISHLLELVGLSEKR--DAYPSQLSGGQKQKQVAGIARALANDPEILLCDEATSDLPKTTG 178
QY 183 ELMTLFFKKLHQS-GMTIVLVTHLMDDDVAEYANQVVMKGRVLVKGKPSDVF 233
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Db 201 ITHNQVVKVKEICNKNVAVNMEDGRIVEKSSIQIFSN 235

Search completed: October 28, 2005, 18:02:54
Job time : 44 secs

Db 179 QIALKKLNQELNLTIVLITHMQVVKVKEICNKNVAVNMEDGRIVEKSSIQIFSN 230

RESULT 15
US-09-107-532A-6490
; Sequence 6490, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bueh
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6490:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...361
; SEQUENCE DESCRIPTION: SEQ ID NO: 6490:
US-09-107-532A-6490

Query Match 26.9%; Score 373; DB 4; Length 361;
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Matches 87; Conservative 46; Mismatches 78; Indels 4; Gaps 4;
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Db 24 AVSDVDTIEKGDVGVGVGAGKSTLVVMNLLQKPTAGEVIVNQTNLSQLSP-KELR 82
Qy 82 QIRKQVGLVFQFAENQIFBETVLKDVAFQNFQGVSEEDAVKTAREKALVGDIESLFDR 141
Db 83 KERKAGWIFQHF-NLMESRTIPDNVDFSLKYSKSKQERRQKVNELLEVLGLEKA-SA 140
Qy 142 SPPELSCGQWRVAIGAILAMEPAIIVLDEPTAGLDPLGRKELMTLPKKLH-QSGMTIVL 200
Db 141 YPKQLSGGQQRVAIRALANEPKVLCDSEATSDLPKTTLQILALIKLNRLQGLTIVL 200
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 17:53:53 ; Search time 167 Seconds
(without alignments)
646.145 Million cell updates/sec

Title: US-09-769-744D-26

Perfect score: 279

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Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

Database : A Geneseq_16Dec04.*

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- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004as.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	267	95.7	279	8	ADK47865 Streptoco
5	267	95.7	280	8	ADR96203 Novel S.
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8	23	8.2	288	5	AB53584 Lactococc
9	22	7.9	279	8	ADK99877 Streptoco
10	22	7.9	279	8	ADK99878 Streptoco
11	22	7.9	279	8	ADK99876 Streptoco
12	22	7.9	279	8	ADK99880 Streptoco
13	22	7.9	279	8	ADK99881 Streptoco
14	22	7.9	279	8	ADK99883 Streptoco
15	22	7.9	279	8	ADK99885 Streptoco
16	22	7.9	279	8	ADK99879 Streptoco
17	22	7.9	279	8	ADK99884 Streptoco
18	22	7.9	279	8	ADK99882 Streptoco
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20	22	7.9	280	5	ABP26997 Streptoco
21	22	7.9	280	6	ABU46897 Protein e
22	22	7.9	280	6	ABU44574 Protein e
23	22	7.9	280	6	ADK99875 Streptoco
24	19	6.8	276	8	AD44624 Bacterial
25	18	6.5	180	2	AAW44388 Vancomyci

26	18	6.5	272	6	ABU17390	Abu17390 Protein e
27	18	6.5	284	7	ADC96403	E. faeciu
28	18	6.5	288	5	AB47921	Listeria
29	18	6.5	288	6	ABU32554	Protein e
30	18	6.5	289	6	ABU29735	Protein e
31	18	6.5	293	6	ABU18769	Protein e
32	17	6.1	289	4	AAU34952	Enterococ
33	17	6.1	289	6	ABU29324	Protein e
34	17	6.1	316	7	ADH86847	Enterococ
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37	13	4.7	294	6	ADB66404	Alloioioc
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39	11	3.9	253	8	ADS44456	Bacterial
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48	11	3.9	547	4	AAU57027	Propionib
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50	11	3.9	592	6	ABU11759	Human MDD
51	11	3.9	856	6	ADA5361	Human tra
52	11	3.9	1157	8	ADP99144	Human tra
53	11	3.9	1400	7	ADL33323	Human tra
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56	11	3.9	1585	5	AAE21186	Human TRI
57	11	3.9	1624	5	ABB81576	Human ATP
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61	10	3.6	141	6	ABM39481	Propionib
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63	10	3.6	198	4	AAAB61432	ABC trans
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66	10	3.6	198	7	ADP65524	ATP-bind
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68	10	3.6	226	8	ADN26297	Bacterial
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71	10	3.6	268	5	ABB47338	Listeria
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75	10	3.6	286	6	ABU43237	Protein e
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77	10	3.6	288	5	ABP38447	Staphyloc
78	10	3.6	288	6	ABU25536	Protein e
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80	10	3.6	292	4	AAAB76685	Corynebac
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85	10	3.6	312	8	ADN26970	Bacterial
86	10	3.6	320	4	AAU59476	Protonib
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90	10	3.6	551	8	ADS27560	Bacterial
91	10	3.6	601	8	ADS28154	Bacterial
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93	10	3.6	898	8	ADS13002	TRICH-25.
94	10	3.6	1458	8	ABM85034	Human dia
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105	10	3.6	1581	8	ADR99166	Adr99166 ATP-bindi	178	8	2.9	297	8	ADN21934	Adn21934 Bacterial
106	10	3.6	1592	5	AAE21161	Aae21161 Human TRI	179	8	2.9	298	8	ADN25944	Adn25944 Bacterial
107	10	3.6	1595	5	ADH48754	Adh48754 NOV14 pro	180	8	2.9	300	8	ADN24691	Adn24691 Bacterial
108	10	3.6	1621	6	ADA20301	Ada20301 Human ATP	181	8	2.9	306	8	ADS29019	Ads29019 Bacterial
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113	9	3.2	196	8	ADS30081	Ads30081 Bacterial	186	8	2.9	380	8	ADN26984	Adn26984 Bacterial
114	9	3.2	273	4	AAU34054	Aau34054 Staphyloc	187	8	2.9	384	5	ABP28071	Abp28071 Streptoco
115	9	3.2	283	6	ABU18623	Abu18623 Protein e	188	8	2.9	384	5	ABP26058	Abp26058 Streptoco
116	9	3.2	284	7	ADE86092	Ade86092 Streptomy	189	8	2.9	384	8	ADN26231	Adn26231 Bacterial
117	9	3.2	285	6	ABU24825	Abu24825 Protein e	190	8	2.9	385	6	ABU01832	Abu01832 S. pneumo
118	9	3.2	285	8	ADN18357	Adn18357 Bacterial	191	8	2.9	385	8	ADR95135	Adr95135 Novel S.
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122	9	3.2	288	8	ADS28106	Ads28106 Bacterial	195	8	2.9	475	2	AAU08961	Aau08961 A. gossyp
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124	9	3.2	292	8	ADS21825	Ads21825 Bacterial	197	8	2.9	479	8	ADS28930	Ads28930 Bacterial
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131	9	3.2	565	5	ABB53631	Abb53631 Lactococc	204	8	2.9	555	2	AAW89799	Aaw89799 Staphyloc
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136	9	3.2	595	7	ADF05723	Adf05723 Bacterial	209	8	2.9	567	8	ADS08129	Ads08129 Staphyloc
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138	9	3.2	611	5	ABB53567	Abb53567 Lactococc	211	8	2.9	572	6	ADB12519	Adb12519 Alloiococ
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160	8	2.9	243	4	AAU91098	Aau91098 C glutami	233	8	2.9	650	5	ABB48907	Abb48907 Listeria
161	8	2.9	243	8	ADQ59493	Adq59493 Human can	234	8	2.9	650	6	ABU32711	Abu32711 Protein e
162	8	2.9	248	8	ADN18335	Adn18335 Bacterial	235	8	2.9	673	8	ADS28635	Ads28635 Bacterial
163	8	2.9	250	5	ABP26471	Abp26471 Streptoco	236	8	2.9	674	8	ADN28161	Adn28161 Bacterial
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252	7	2.5	10	4	AAJ00342	AaJ00342	Hepatitis	325	7	2.5	145	4	AAAB95695	Aab95695	Human tes
253	7	2.5	10	4	AAJ01508	AaJ01508	Hepatitis	326	7	2.5	145	4	ABAB95695	Ab95695	Human tes
254	7	2.5	10	4	AAJ00505	AaJ00505	Hepatitis	327	7	2.5	148	6	ADA36713	Ada36713	Acinetoba
255	7	2.5	11	4	AAJ00753	AaJ00753	Hepatitis	328	7	2.5	149	6	ABM69510	Abm69510	Photorhab
256	7	2.5	11	4	AAJ01094	AaJ01094	Hepatitis	329	7	2.5	151	8	ADR32314	Adr32314	Renilla r
257	7	2.5	11	4	AAJ02506	AaJ02506	Hepatitis	330	7	2.5	152	8	ADR32312	Adr32312	Renilla r
258	7	2.5	11	4	AAJ02717	AaJ02717	Hepatitis	331	7	2.5	157	2	AAAB33886	Aaw33886	Flea sali
259	7	2.5	11	4	AAJ02236	AaJ02236	Hepatitis	332	7	2.5	157	2	AAAB82360	Aaw82360	Flea sali
260	7	2.5	11	4	AAJ01939	AaJ01939	Hepatitis	333	7	2.5	157	2	AAAB30886	Aau30886	Novel hum
261	7	2.5	11	8	ADL26022	AdL26022	Synthetic	334	7	2.5	158	5	ABAB77260	Abb77260	HCV bait
262	7	2.5	15	8	ADL25996	AdL25996	Synthetic	335	7	2.5	161	8	ADNA47187	Adn47187	Thermococ
263	7	2.5	15	8	ADL25997	AdL25997	Synthetic	336	7	2.5	166	4	AAAB00974	Aam00974	Human bon
264	7	2.5	15	8	ADL25999	AdL25999	Synthetic	337	7	2.5	174	6	ABU01226	Abu01226	S. pneumo
265	7	2.5	15	8	ADL26000	AdL26000	Synthetic	338	7	2.5	176	4	AAAB91745	Aam91745	Human imm
266	7	2.5	15	8	ADL25995	AdL25995	Synthetic	339	7	2.5	176	4	AAAB18425	Aau18425	Human end
267	7	2.5	15	8	ADL26025	AdL26025	Synthetic	340	7	2.5	176	8	ADS21408	AdS21408	Bacterial
268	7	2.5	15	8	ADL25998	AdL25998	Synthetic	341	7	2.5	185	2	AAAY02369	Aay02369	Polypepti
269	7	2.5	15	8	ADL26023	AdL26023	Synthetic	342	7	2.5	187	5	ABP03719	Abp03719	Human ORF
270	7	2.5	15	8	ADL26024	AdL26024	Synthetic	343	7	2.5	189	8	ADN26887	Adn26887	Bacterial
271	7	2.5	15	8	ADL26026	AdL26026	Synthetic	344	7	2.5	189	8	ADN26887	Adn26887	Bacterial
272	7	2.5	15	8	ADL26027	AdL26027	Synthetic	345	7	2.5	192	6	ADB17009	Adb17009	ABC trans
273	7	2.5	15	8	ADL26028	AdL26028	Synthetic	346	7	2.5	193	4	AAAB81943	Aag81943	S. epider
274	7	2.5	18	2	AAAB13344	Aar13344	P1223 HCV	347	7	2.5	194	5	ABAB77262	Abb77262	HCV bait
275	7	2.5	18	2	AAAB33867	Aar33867	Polypepti	348	7	2.5	197	4	AAAB76744	Aab76744	Corynebac
276	7	2.5	20	8	ADM29122	Adm29122	Hepatitis	349	7	2.5	197	8	ADS44690	AdS44690	Bacterial
277	7	2.5	24	2	AAAB60137	Aaw60137	Mycobacte	350	7	2.5	198	7	ABO63975	AbO63975	Klebsiell
278	7	2.5	24	2	AAAB14884	Aay14884	N-termina	351	7	2.5	202	6	ABU21011	Abu21011	Protein e
279	7	2.5	24	5	ABAB73490	Abb73490	M vaccae	352	7	2.5	202	8	ADS30362	AdS30362	Bacterial
280	7	2.5	28	5	ABAB77227	Abb77227	Selected	353	7	2.5	205	4	AAU03136	Aau03136	Streptoco
281	7	2.5	30	5	AAAB84680	Aau84680	HCV HepC1	354	7	2.5	207	2	AAAB25859	Aar25859	HCV poly
282	7	2.5	30	5	AAAB84679	Aau84679	HCV HepC1	355	7	2.5	207	2	AAAB25859	Aar25859	HCV poly
283	7	2.5	34	8	ADL34965	Adl34965	Hepatitis	356	7	2.5	208	8	ADN28387	Adn28387	Hepatitis
284	7	2.5	40	2	AAAB51162	Aar51162	Peptide (357	7	2.5	213	2	AAAB20717	Aar20717	C10-23 NA
285	7	2.5	41	8	ADL26412	AdL26412	Synthetic	358	7	2.5	213	8	ADL05055	AdL05055	M. catarr
286	7	2.5	41	8	ADL26413	AdL26413	Synthetic	359	7	2.5	215	2	AAAB26866	Aaw26866	L. cornic
287	7	2.5	43	8	ADL05293	AdL05293	Staphyloc	360	7	2.5	216	6	ABM65399	Abm65399	Propionib
288	7	2.5	49	2	AAAB33866	Aar33866	Polypepti	361	7	2.5	220	8	ADN26973	Adn26973	Bacterial
289	7	2.5	50	2	AAAB33350	Aar33350	P1192 HCV	362	7	2.5	221	6	AAAB25881	Aar25881	HK6, 9/20
290	7	2.5	67	4	ABG01599	Abg01599	Novel hum	363	7	2.5	221	6	ABU20088	Abu20088	Protein e
291	7	2.5	70	5	ABP10464	Abp10464	Human ORF	364	7	2.5	222	6	ABP81430	Abp81430	Streptoco
292	7	2.5	71	3	AAAG00410	Aag00410	Human sec	365	7	2.5	224	4	AAAG93172	Aag93172	C glutami
293	7	2.5	72	3	AAAB65113	Aay65113	Human 5'	366	7	2.5	224	2	AAAB80708	Aaw80708	S. pneumo
294	7	2.5	80	2	AAAB04874	Aaw04874	DNA fragm	367	7	2.5	228	6	ABU37611	Abu37611	N. gonorr
295	7	2.5	82	2	AAAB24596	Aaw24596	Hepatitis	368	7	2.5	228	6	ABP79323	Abp79323	Protein e
296	7	2.5	82	2	AAAB44815	Aaw44815	Hepatitis	369	7	2.5	228	6	ABP79323	Abp79323	N. gonorr
297	7	2.5	84	5	ABP05993	Abp05993	Human ORF	370	7	2.5	229	2	AAAB98349	Aar98349	Novel S.
298	7	2.5	88	7	ADP089170	Adp089170	Ribosomal	371	7	2.5	230	8	ADN17519	Adn17519	Bacterial
299	7	2.5	89	8	ADP30531	Adp30531	Bacterial	372	7	2.5	232	6	ABM71118	Abm71118	Staphyloc
300	7	2.5	98	3	AAAB65425	Aay65425	Human 5'	373	7	2.5	232	6	ADN25104	Adn25104	Bacterial
301	7	2.5	102	4	AAAB67310	Aab67310	ABC trans	374	7	2.5	233	3	AAAY75763	Aay75763	Neisseria
302	7	2.5	102	4	AAAB45738	Aau45738	Propionib	375	7	2.5	233	8	ADL05394	AdL05394	M. catarr
303	7	2.5	102	6	ABM42257	Abm42257	Propionib	376	7	2.5	233	8	ADL05394	AdL05394	M. catarr
304	7	2.5	108	7	ADP36598	Adp36598	Human NOV	377	7	2.5	233	8	ADL05394	AdL05394	M. catarr
305	7	2.5	109	7	ADP95172	Adp95172	Bacteriop	378	7	2.5	235	5	ABP30426	Abp30426	Bacterial
306	7	2.5	111	3	AAAB65371	Aay65371	Human 5'	379	7	2.5	235	6	ABU42193	Abu42193	Protein e
307	7	2.5	112	3	AAAB15670	Aag15670	Arabidops	380	7	2.5	235	6	ABU42193	Abu42193	Protein e
308	7	2.5	114	4	AAAB31975	Aau31975	Novel hum	381	7	2.5	235	7	ADM26338	Adm26338	Hypather
309	7	2.5	116	4	ABG04902	Abg04902	Novel hum	382	7	2.5	235	8	ADS30303	AdS30303	Bacterial
310	7	2.5	117	6	ADP77747	Adp77747	Partial:s	383	7	2.5	237	6	ADL12443	Adl12443	Alloioococ
311	7	2.5	121	7	ADK68144	Adk68144	Novel NOV	384	7	2.5	238	6	ADA89516	Ada89516	Staphyloc
312	7	2.5	121	8	ADR49133	Adr49133	Human NOV	385	7	2.5	246	1	AAAB92030	Aap92030	Sequence
313	7	2.5	125	1	AAAB12263	Aay12263	Human 5'	386	7	2.5	247	6	ABU21727	Abu21727	Protein e
314	7	2.5	125	7	ADD18252	Adl18252	Human mol	387	7	2.5	249	4	AAAB92340	Aag92340	C. glutami
315	7	2.5	125	7	ADK68140	Adk68140	Novel NOV	388	7	2.5	251	5	ABP65924	Abp65924	Bifidobac
316	7	2.5	125	8	ADR49129	Adr49129	Human NOV	389	7	2.5	251	6	ADL12441	Adl12441	Alloioococ
317	7	2.5	127	6	ADA55239	Ada55239	Human pro	390	7	2.5	251	7	ADF04354	Adf04354	Bacterial

391	7	2.5	252	4	AAM86393	Aam86393 Human imm	464	7	2.5	280	5	ABP38624	Abp38624 Staphyloc
392	7	2.5	252	4	AAM91743	Aam91743 Human imm	465	7	2.5	280	8	ADS05124	Ads05124 Staphyloc
393	7	2.5	252	4	AAM42386	Aam42386 Human pol	466	7	2.5	281	2	AAY37001	Aay37001 Chlamydia
394	7	2.5	252	4	AU18422	Au18422 Human end	467	7	2.5	281	6	ABU01985	Abu01985 S. pneumo
395	7	2.5	252	4	AU18423	Au18423 Human end	468	7	2.5	281	7	ADH86577	Adh86577 Enterococ
396	7	2.5	252	4	ABO67564	AbO67564 Klebsiell	469	7	2.5	282	2	AAW01956	Aaw01956 Hepatitis
397	7	2.5	253	2	AAR20609	Aar20609 C11-7 NAN	470	7	2.5	282	6	ABP70431	Abp70431 Amino aci
398	7	2.5	253	2	AAR60321	Aar60321 NANBHV NS	471	7	2.5	282	2	ABO62650	AbO62650 Klebsiell
399	7	2.5	253	8	ADN46403	Adn46403 Thermococ	472	7	2.5	284	2	AAR20614	Aar20614 C10-16 NA
400	7	2.5	257	4	ABBS8273	Abbs8273 Drosophil	473	7	2.5	284	2	AAR50071	Aar50071 NANBH vir
401	7	2.5	258	8	ADS29521	Ads29521 Bacterial	474	7	2.5	284	2	AAY34801	Aay34801 Chlamydia
402	7	2.5	259	7	ADP06451	Adp06451 Bacterial	475	7	2.5	284	8	ADJ81676	Adj81676 Non-A-non
403	7	2.5	260	8	ADN22410	Adn22410 Bacterial	476	7	2.5	285	4	ABE67316	AbE67316 Gene #2 p
404	7	2.5	261	4	AAU18298	Aau18298 Human end	477	7	2.5	285	6	ABU24615	Abu24615 Protein e
405	7	2.5	261	6	ABM71008	Abm71008 Staphyloc	478	7	2.5	286	2	AAR40222	Aar40222 Hepatitis
406	7	2.5	263	5	ABBY7261	Abb7261 HCV bait	479	7	2.5	290	5	ABP38428	Abp38428 Staphyloc
407	7	2.5	263	7	ADE36629	Ade36629 Human NOV	480	7	2.5	290	8	ADS07099	AdS07099 Staphyloc
408	7	2.5	263	7	ADE36622	Ade36622 Plasmid p	481	7	2.5	291	6	ADA77739	Ada77739 Wild type
409	7	2.5	263	7	ADE36596	Ade36596 Human NOV	482	7	2.5	291	7	ADC94578	Adc94578 E. faeciu
410	7	2.5	266	1	AAP90147	Aap90147 Sequence	483	7	2.5	291	8	ADS30591	Ads30591 Bacterial
411	7	2.5	266	1	AAR62863	Aar62863 Korean-ty	484	7	2.5	292	6	ADA33607	Ada33607 Acinetoba
412	7	2.5	266	2	AAR90932	Aar90932 HCV antig	485	7	2.5	293	4	AAG91103	Aag91103 Corynebac
413	7	2.5	266	2	AAR90932	Aar90932 HCV antig	486	7	2.5	293	4	AAG91103	Aag91103 C glutami
414	7	2.5	266	5	ABP25447	Abp25447 Streptoco	487	7	2.5	293	5	ABP26437	Abp26437 Streptoco
415	7	2.5	267	6	ABM68503	Abm68503 Phototrab	488	7	2.5	293	7	ADL65435	Adl65435 C. Glutam
416	7	2.5	267	8	ADI39249	Adi39249 S. hygro	489	7	2.5	294	3	AAE69649	Aae69649 Hepatitis
417	7	2.5	269	4	AAU66854	Aau66854 Propionib	490	7	2.5	294	6	ABU48972	Abu48972 Protein e
418	7	2.5	269	6	ABM63373	Abm63373 Propionib	491	7	2.5	295	6	ABR63601	Abr63601 Hepatitis
419	7	2.5	269	6	ABU43238	Abu43238 Protein e	492	7	2.5	295	6	ABR63601	Abr63601 Hepatitis
420	7	2.5	269	6	ABU16230	Abu16230 Protein e	493	7	2.5	297	8	ADS22519	Ads22519 Bacterial
421	7	2.5	269	6	ADA77740	Ada77740 Regions o	494	7	2.5	297	8	ADN27327	Adn27327 Bacterial
422	7	2.5	272	2	AAR14545	Aar14545 Encoded b	495	7	2.5	298	6	ABU41764	Abu41764 Protein e
423	7	2.5	272	2	AAR14356	Aar14356 HCV prote	496	7	2.5	298	8	ADQ76693	Adq76693 Human KIM
424	7	2.5	272	2	AAR68546	Aar68546 Hepatitis	497	7	2.5	298	8	ADS27088	Ads27088 Bacterial
425	7	2.5	272	2	AAW01686	Aaw01686 HCV prote	498	7	2.5	298	8	ADS41991	Ads41991 Bacterial
426	7	2.5	272	2	AAW46396	Aaw46396 Amino aci	499	7	2.5	299	2	AAS68549	Aas68549 Hepatitis
427	7	2.5	272	2	AAW97608	Aaw97608 Amino aci	500	7	2.5	299	2	AAS68549	Aas68549 Hepatitis
428	7	2.5	272	6	ABO27019	AbO27019 Hepatitis	501	7	2.5	299	2	AAW01699	Aaw01699 Protein d
429	7	2.5	273	2	ADA07873	Ada07873 Hepatitis	502	7	2.5	299	2	AAW01697	Aaw01697 Protein d
430	7	2.5	273	2	AAR50072	Aar50072 NANBH vir	503	7	2.5	299	2	AAW46386	Aaw46386 Protease
431	7	2.5	273	5	ABP38796	Abp38796 Staphyloc	504	7	2.5	299	2	AAW97598	Aaw97598 Protein s
432	7	2.5	274	8	ADJ81677	Adj81677 Non-A-non	505	7	2.5	299	2	AAW97598	Aaw97598 Protein s
433	7	2.5	274	4	AAU34053	Aau34053 Staphyloc	506	7	2.5	299	2	AAW97600	Aaw97600 Protein s
434	7	2.5	274	6	ABU36368	Abu36368 Protein e	507	7	2.5	299	6	ABO27063	AbO27063 Hepatitis
435	7	2.5	274	6	ABU35572	Abu35572 Protein e	508	7	2.5	299	8	ADA07942	Ada07942 Hepatitis
436	7	2.5	275	6	ADA33530	Ada33530 Acinetoba	509	7	2.5	300	3	AAE69648	Aae69648 Phototrab
437	7	2.5	277	4	AUA43271	Aua43271 Propionib	510	7	2.5	300	6	ABM68949	Abm68949 Phototrab
438	7	2.5	277	6	ABM39790	Abm39790 Propionib	511	7	2.5	300	7	ADH85848	Adh85848 Enterococ
439	7	2.5	277	6	ABU25559	Abu25559 Protein e	512	7	2.5	300	8	ADQ15292	AdQ15292 Hepatitis
440	7	2.5	278	2	AAR84358	Aar84358 Hepatitis	513	7	2.5	300	8	ADS23576	Ads23576 Bacterial
441	7	2.5	278	5	ABBY7259	Abb7259 HCV bait	514	7	2.5	300	8	ADS28908	Ads28908 Bacterial
442	7	2.5	278	6	ABU27455	Abu27455 Protein e	515	7	2.5	301	2	AAW01049	Aaw01049 Product o
443	7	2.5	278	8	ADO15289	Ado15289 Hepatitis	516	7	2.5	301	3	AAE69648	Aae69648 Phototrab
444	7	2.5	279	3	AAE69648	Aae69648 Phototrab	517	7	2.5	301	3	AAE69648	Aae69648 Phototrab
445	7	2.5	279	3	AAE69648	Aae69648 Phototrab	518	7	2.5	301	4	AAE69648	Aae69648 Phototrab
446	7	2.5	279	3	AAE69648	Aae69648 Phototrab	519	7	2.5	301	4	AAE69648	Aae69648 Phototrab
447	7	2.5	279	3	AAE69648	Aae69648 Phototrab	520	7	2.5	301	4	AAE69648	Aae69648 Phototrab
448	7	2.5	279	3	AAE69648	Aae69648 Phototrab	521	7	2.5	301	4	AAE69648	Aae69648 Phototrab
449	7	2.5	279	3	AAE69648	Aae69648 Phototrab	522	7	2.5	301	4	AAE69648	Aae69648 Phototrab
450	7	2.5	279	3	AAE69648	Aae69648 Phototrab	523	7	2.5	301	5	ABG32775	Abg32775 Human TH
451	7	2.5	279	3	AAE69648	Aae69648 Phototrab	524	7	2.5	301	5	ABG32775	Abg32775 Human TH
452	7	2.5	279	3	AAE69648	Aae69648 Phototrab	525	7	2.5	301	6	ABP70445	Abp70445 Amino aci
453	7	2.5	279	3	AAE69648	Aae69648 Phototrab	526	7	2.5	301	6	ABP70445	Abp70445 Amino aci
454	7	2.5	279	3	AAE69648	Aae69648 Phototrab	527	7	2.5	301	6	ABG73718	Abg73718 Human TH
455	7	2.5	279	3	AAE69648	Aae69648 Phototrab	528	7	2.5	301	7	ADB37497	AdB37497 Human TH
456	7	2.5	279	3	AAE69648	Aae69648 Phototrab	529	7	2.5	301	7	ABR82712	Abr82712 Human TIM
457	7	2.5	279	3	AAE69648	Aae69648 Phototrab	530	7	2.5	301	7	ABR82712	Abr82712 Human TIM
458	7	2.5	279	4	ABG25857	Abg25857 Novel hum	531	7	2.5	301	7	ADM68638	Adm68638 Different
459	7	2.5	279	5	ABBA47922	Abba47922 Listeria	532	7	2.5	301	8	ADH80727	Adh80727 Human pol
460	7	2.5	279	6	ABU32730	Abu32730 Protein e	533	7	2.5	301	8	ADQ20503	Ado20503 Human PRO
461	7	2.5	279	6	ABU24207	Abu24207 Protein e	534	7	2.5	301	8	ADQ95878	Adq95878 T cell ac
462	7	2.5	279	6	ADB06406	Adb06406 Alloecoc	535	7	2.5	301	8	ADQ95876	Adq95876 T cell ac
463	7	2.5	280	4	AAB96282	Aab96282 Putative	536	7	2.5	302	8	ADN26506	Adn26506 Bacterial

537	7	2.5	302	8	ADS25912	AdS25912 Bacterial
538	7	2.5	304	6	ABM67587	ABM67587 Phototab
539	7	2.5	304	8	ADS26336	AdS26336 Bacterial
540	7	2.5	304	8	ADS41984	AdS41984 Bacterial
541	7	2.5	304	8	ADS26703	AdS26703 Bacterial
542	7	2.5	305	6	ABP70430	ABP70430 Amino aci
543	7	2.5	306	4	AAU36640	AAU36640 Staphyloc
544	7	2.5	306	4	ABB62221	ABb62221 Drosophil
545	7	2.5	306	6	ABM73365	ABm73365 Staphyloc
546	7	2.5	306	8	ADN26437	Adn26437 Bacterial
547	7	2.5	306	8	ADN23044	Adn23044 Bacterial
548	7	2.5	307	2	AAK29859	AAr29859 HCV NS2-N
549	7	2.5	307	2	AAK29858	AAr29858 HCV NS2-N
550	7	2.5	307	2	AAK29857	AAr29857 HCV NS2-N
551	7	2.5	307	2	AAK29843	AAr29843 HCV NS2-N
552	7	2.5	307	2	AAW38334	AAw38334 Rat kidne
553	7	2.5	307	4	AAAB96120	AAb96120 Putative
554	7	2.5	307	6	ABU38602	ABu38602 Protein e
555	7	2.5	308	4	AAU34619	AAu34619 E. coli c
556	7	2.5	308	4	AG98922	AGg98922 E. coli g
557	7	2.5	308	4	AAU29364	AAu29364 Novel mar
558	7	2.5	308	6	ABU28679	ABu28679 Protein e
559	7	2.5	308	6	ABU28137	ABu28137 Protein e
560	7	2.5	308	6	ABU47287	ABu47287 Protein e
561	7	2.5	308	8	ADN17599	Adn17599 Bacterial
562	7	2.5	308	8	ADN24970	Adn24970 Bacterial
563	7	2.5	308	8	ADN23041	Adn23041 Bacterial
564	7	2.5	308	8	ADN18052	Adn18052 Bacterial
565	7	2.5	308	8	ADN18240	Adn18240 Bacterial
566	7	2.5	309	7	ABO72458	ABo72458 Pseudomon
567	7	2.5	309	8	ADN22211	Adn22211 Bacterial
568	7	2.5	309	8	ADS26487	AdS26487 Bacterial
569	7	2.5	310	8	ADM94402	Adm94402 Wheat MRP
570	7	2.5	311	2	AAK27165	AAr27165 Recombina
571	7	2.5	311	2	AAK48550	AAr48550 Recombina
572	7	2.5	311	2	AAK74079	AAr74079 Renilla r
573	7	2.5	311	2	AAK39947	AAy39947 R. muller
574	7	2.5	311	3	AAK84836	AAy84836 Amino aci
575	7	2.5	311	3	AAK70363	AAy70363 Renilla l
576	7	2.5	311	3	AAK44791	AAy44791 Soybean A
577	7	2.5	311	3	AAK46265	AAg46265 Arabidops
578	7	2.5	311	4	ABB47282	ABb47282 Enterococ
579	7	2.5	311	5	AAE13381	AAe13381 Renilla m
580	7	2.5	311	5	AAE19116	AAe19116 Renilla r
581	7	2.5	311	5	AAE19115	AAe19115 Renilla r
582	7	2.5	311	5	AAU11515	AAu11515 Renilla l
583	7	2.5	311	5	ABB97171	ABb97171 R renifor
584	7	2.5	311	5	ABB97172	ABb97172 R renifor
585	7	2.5	311	5	ABB97170	ABb97170 R renifor
586	7	2.5	311	5	ABB97173	ABb97173 R renifor
587	7	2.5	311	5	ABB49854	ABb49854 Listeria
588	7	2.5	311	6	ABU02212	ABu02212 S. pneumo
589	7	2.5	311	6	AAO27521	AAo27521 Renilla (
590	7	2.5	311	8	ADK46590	ADk46590 Streptoco
591	7	2.5	311	8	ADM94398	Adm94398 Soybean M
592	7	2.5	311	8	ADM94388	Adm94388 Sea pansy
593	7	2.5	312	6	ABU49846	ABu49846 Protein e
594	7	2.5	312	8	ADS25557	AdS25557 Bacterial
595	7	2.5	312	8	AAK27166	AAr27166 Sequence
596	7	2.5	314	2	AAK48549	AAr48549 Sequence
597	7	2.5	314	3	AAK26343	AAg26343 Arabidops
598	7	2.5	314	3	AG43058	AGg43058 Arabidops
599	7	2.5	314	3	AG28959	AGg28959 Arabidops
600	7	2.5	314	4	AAK51159	AAk51159 Renilla r
601	7	2.5	314	4	AAK96594	AAk96594 Putative
602	7	2.5	314	5	ABB82055	ABb82055 R.f reinfo
603	7	2.5	314	5	AAE13366	AAe13366 Renilla r
604	7	2.5	314	5	ABE13366	ABe13366 Renilla r
605	7	2.5	314	6	ADA14766	ADa14766 Sea pansy
606	7	2.5	314	6	ABG73286	ABg73286 Renilla r
607	7	2.5	314	6	ADA37435	ADa37435 Renilla r
608	7	2.5	314	7	ABW00605	ABw00605 Renilla r
609	7	2.5	314	8	ADM80595	Adm80595 Luciferas

610	7	2.5	314	8	ADR43968	AdR43968 Renilla r
611	7	2.5	314	8	AGS28016	AGs28016 Bacterial
612	7	2.5	314	8	ADS43192	AdS43192 Bacterial
613	7	2.5	314	8	ADS29090	AdS29090 Bacterial
614	7	2.5	314	8	ADS42552	AdS42552 Bacterial
615	7	2.5	315	2	AAK28466	AAk28466 Sequence
616	7	2.5	315	6	ABU44977	ABu44977 Protein e
617	7	2.5	315	6	ABU432374	ABu432374 Protein e
618	7	2.5	315	6	ADH88564	ADh88564 Acinetoba
619	7	2.5	315	6	ADH85279	ADh85279 Novel S.
620	7	2.5	315	8	ADR95279	AdR95279 Novel S.
621	7	2.5	316	6	ABRS3222	ABrS3222 Protein s
622	7	2.5	316	7	ADF05899	AdF05899 Bacterial
623	7	2.5	316	7	ADK63718	ADk63718 Disease t
624	7	2.5	316	8	ADK41768	ADk41768 Bacterial
625	7	2.5	316	8	ADS29721	AdS29721 Bacterial
626	7	2.5	317	6	ABU42860	ABu42860 Protein e
627	7	2.5	317	6	ABO64109	ABo64109 Klebsiell
628	7	2.5	318	3	AAK43898	AAy43898 Amino aci
629	7	2.5	318	3	AAK43900	AAy43900 Amino aci
630	7	2.5	318	3	AAK43899	AAy43899 Amino aci
631	7	2.5	318	3	AAK43894	AAy43894 Amino aci
632	7	2.5	318	3	AAK43895	AAy43895 Amino aci
633	7	2.5	318	5	ABP66268	ABp66268 Bifidobac
634	7	2.5	319	5	ABP39043	ABp39043 Staphyloc
635	7	2.5	319	5	ABB55189	ABb55189 Lactococc
636	7	2.5	319	5	ABB55242	ABb55242 Lactococc
637	7	2.5	319	6	ABU43920	ABu43920 Protein e
638	7	2.5	319	6	ABO61599	ABo61599 Klebsiell
639	7	2.5	319	8	ADS07028	AdS07028 Staphyloc
640	7	2.5	323	4	AAK96077	AAk96077 Putative
641	7	2.5	323	7	ABO65979	ABo65979 Klebsiell
642	7	2.5	324	6	ABM71022	ABm71022 Staphyloc
643	7	2.5	326	3	AAK43897	AAy43897 Amino aci
644	7	2.5	326	3	AAK43896	AAy43896 Amino aci
645	7	2.5	326	6	AAK46264	AAg46264 Arabidops
646	7	2.5	326	6	ABU28141	ABu28141 Protein e
647	7	2.5	327	7	ABO65446	ABo65446 Klebsiell
648	7	2.5	328	2	AAK41437	AAr41437 PT-NANBH
649	7	2.5	328	5	ABP38817	ABp38817 Staphyloc
650	7	2.5	328	6	ABU15017	ABu15017 Protein e
651	7	2.5	328	6	AAW26162	AAw26162 Fragment
652	7	2.5	330	8	ADJ56872	ADj56872 Corn TTG
653	7	2.5	330	8	ADJ42868	AdJ42868 Bacterial
654	7	2.5	333	5	ABB49315	ABb49315 Listeria
655	7	2.5	333	6	ABU32615	ABu32615 Protein e
656	7	2.5	334	2	AAW38336	AAw38336 Human kid
657	7	2.5	334	4	AAK84657	AAk84657 Amino aci
658	7	2.5	334	6	AAO26679	AAo26679 KIM-1 rel
659	7	2.5	334	6	ADO29371	Ado29371 Mouse GPC
660	7	2.5	334	8	ADO27736	Ado27736 Bacterial
661	7	2.5	334	8	ADG76696	ADg76696 Human kid
662	7	2.5	335	7	ABO72091	ABo72091 Pseudomon
663	7	2.5	336	3	AAK46263	AAg46263 Arabidops
664	7	2.5	336	4	ABG25968	ABg25968 Novel hum
665	7	2.5	338	8	ADM94350	Adm94350 Corn P-gl
666	7	2.5	339	3	AAK84839	AAk84839 Amino aci
667	7	2.5	339	3	AAK84838	AAk84839 Amino aci
668	7	2.5	339	3	AAK84841	AAk84841 Amino aci
669	7	2.5	339	3	AAK84840	AAk84840 Amino aci
670	7	2.5	339	3	AAK84837	AAk84837 Human Pro
671	7	2.5	339	7	ADK46755	ADk46755 Rat Prote
672	7	2.5	339	7	ADK46755	ADk46755 Rat Prote
673	7	2.5	339	7	ADE55552	AdE55552 Rat Prote
674	7	2.5	339	7	ADE55554	AdE55554 Human Pro
675	7	2.5	339	7	ADE36618	AdE36618 Plasmid p
676	7	2.5	339	7	ADE36592	AdE36592 Human NOV
677	7	2.5	339	8	ADQ17619	ADq17619 Human sof
678	7	2.5	339	8	ABM81054	ABm81054 Tumour-as
679	7	2.5	340	4	AAK91479	AAk91479 C Glutam
680	7	2.5	341	6	ABU31733	ABu31733 Protein e
681	7	2.5	341	6	ABU14858	ABu14858 Protein e
682	7	2.5	341	6	ABU14858	ABu14858 Protein e

683	7	2.5	343	6	ABU02418	Abu02418 S. pneumo	756	7	2.5	377	6	ABM71759	Abm71759 Staphyloc
684	7	2.5	343	6	ABP81463	Abp81463 Streptoco	757	7	2.5	377	7	ADG30683	Adg30683 Xanthomon
685	7	2.5	344	6	ABU33636	Abu33636 Protein e	758	7	2.5	378	6	ABU25519	Abu25519 Aspergill
686	7	2.5	344	6	ABU41749	Abu41749 Protein e	759	7	2.5	379	6	ABU17175	Abu17175 Protein e
687	7	2.5	344	6	ABU38248	Abu38248 Protein e	760	7	2.5	381	6	ABU44734	Abu44734 Protein e
688	7	2.5	344	6	ABU37499	Abj37499 HCV relat	761	7	2.5	383	5	ABU05485	Abu05485 M. tuberc
689	7	2.5	344	8	ADJ56875	Adj56875 Soybean T	762	7	2.5	383	6	ABU35880	Abu35880 Protein e
690	7	2.5	345	6	ABU49126	Abu49126 Protein e	763	7	2.5	383	6	ABU34545	Abu34545 Protein e
691	7	2.5	346	3	AGG26342	Agg26342 Arabidops	764	7	2.5	383	6	ADA34135	Ada34135 Acinetoba
692	7	2.5	346	3	AGG28958	Agg28958 Arabidops	765	7	2.5	385	6	ABU39392	Abu39392 Protein e
693	7	2.5	346	3	AGG43057	Agg43057 Arabidops	766	7	2.5	385	8	ABM82071	Abm82071 Tumour-as
694	7	2.5	346	6	ABM67738	Abm67738 Photorhab	767	7	2.5	391	7	ABM85384	Abm85384 Mouse pro
695	7	2.5	346	8	ADN72745	Adn72745 Thale cre	768	7	2.5	391	8	ADG25330	Adg25330 Bacterial
696	7	2.5	346	8	ADN72435	Adn72435 Thale cre	769	7	2.5	399	8	ADS28526	Ads28526 Bacterial
697	7	2.5	347	6	ABP80915	Abp80915 N. gonorr	770	7	2.5	401	6	ABU37916	Abu37916 NOVX prot
698	7	2.5	347	6	ABP80525	Abp80525 N. gonorr	771	7	2.5	404	2	AAW98637	Aaw98637 H. pylori
699	7	2.5	347	6	ABU37729	Abu37729 Protein e	772	7	2.5	408	6	ABP80531	Abp80531 N. gonorr
700	7	2.5	347	6	ABU37572	Abu37572 Protein e	773	7	2.5	408	6	ABP80918	Abp80918 N. gonorr
701	7	2.5	347	8	ADP08174	Adp08174 Neisseria	774	7	2.5	408	8	ADP08173	Adp08173 Neisseria
702	7	2.5	348	7	ABO68187	Abu68187 Pseudomon	775	7	2.5	410	6	ABP78247	Abp78247 N. gonorr
703	7	2.5	349	6	ABU35385	Abu35385 Protein e	776	7	2.5	415	6	ADK48165	Adk48165 Streptoco
704	7	2.5	349	6	ABJ37500	Abj37500 HCV relat	777	7	2.5	416	8	ADJ56873	Adj56873 Corn TIG
705	7	2.5	350	6	ABJ37498	Abj37498 HCV relat	778	7	2.5	418	8	ADM94396	Adm94396 Soybean M
706	7	2.5	351	8	ADN19978	Adn19978 Bacterial	779	7	2.5	424	4	AAAG90605	Aag90605 C glutami
707	7	2.5	352	6	ABU23954	Abu23954 Protein e	780	7	2.5	424	6	ABJ37501	Abj37501 HCV relat
708	7	2.5	352	8	ADN23486	Adn23486 Bacterial	781	7	2.5	424	8	ADS22111	Ads22111 Bacterial
709	7	2.5	353	6	ABJ26119	Abj26119 Aspergill	782	7	2.5	425	8	ADN20956	Adn20956 Bacterial
710	7	2.5	353	2	AAAY48405	Aay48405 Human pro	783	7	2.5	427	5	ABM47845	Abm47845 Listeria
711	7	2.5	354	8	ADN20147	Adn20147 Bacterial	784	7	2.5	427	6	ABU32710	Abu32710 Protein e
712	7	2.5	357	8	ADQ76692	Adq76692 Human KIM	785	7	2.5	429	6	ADR95180	Adr95180 Novel S.
713	7	2.5	358	2	AAAR20715	Aar20715 C10-21 NA	786	7	2.5	431	6	ABU21312	Abu21312 Protein e
714	7	2.5	358	6	ABU49844	Abu49844 Protein e	787	7	2.5	433	6	ABU22103	Abu22103 Protein e
715	7	2.5	358	6	ABU24804	Abu24804 Protein e	788	7	2.5	435	8	ADN21346	Adn21346 Bacterial
716	7	2.5	359	6	ABR58582	Abu58582 Human can	789	7	2.5	443	4	ABU30887	Abu30887 Novel hum
717	7	2.5	359	6	ABP70439	Abp70439 Amino aci	790	7	2.5	445	4	ABBG3068	Abbg3068 Drosophil
718	7	2.5	359	6	ABP70441	Abp70441 Amino aci	791	7	2.5	445	8	ADR96700	Adr96700 Drosophil
719	7	2.5	359	6	ABP70438	Abp70438 Amino aci	792	7	2.5	447	4	ABG24991	Abg24991 Novel hum
720	7	2.5	359	6	ABR48174	Abu48174 Human bla	793	7	2.5	451	4	ABG16737	Abg16737 Novel hum
721	7	2.5	359	6	AAO26680	Aao26680 KIM-1 rel	794	7	2.5	452	6	ADR27650	Adr27650 Protein e
722	7	2.5	359	7	ADE36594	Ade36594 Human NOV	795	7	2.5	452	8	ADR27657	Adr27657 OB-RGRP L
723	7	2.5	359	8	ADN38984	Adn38984 Cance/an	796	7	2.5	453	5	ADP27669	Adp27669 MYO47 LUC
724	7	2.5	359	8	ADQ76690	Adq76690 Human kid	797	7	2.5	453	5	ABP65641	Abp65641 Bifidobac
725	7	2.5	360	6	ABU25180	Abu25180 Protein e	798	7	2.5	456	8	ADS29239	Ads29239 Bacterial
726	7	2.5	361	3	AAAY32202	Aay32202 Human rec	799	7	2.5	460	8	ADS41814	Ads41814 Bacterial
727	7	2.5	361	4	AAAY93218	Aay93218 Human pol	800	7	2.5	465	2	AAW31885	Aaw31885 HCV-1 non
728	7	2.5	361	4	AAE03646	Aae03646 Human ext	801	7	2.5	465	8	ADQ76695	Adq76695 Mouse kim
729	7	2.5	361	6	ABR64256	Abu64256 Angiogene	802	7	2.5	473	5	AAAM50076	Aam50076 HCV NS3 h
730	7	2.5	361	7	ADO36769	Ado36769 Murine LA	803	7	2.5	489	6	ADBO8674	Adbo8674 Alloiococ
731	7	2.5	361	8	ADL30591	Adl30591 Human pro	804	7	2.5	490	7	ABO78464	Abu78464 Pseudomon
732	7	2.5	361	8	ADQ19404	Adq19404 Human sof	805	7	2.5	490	8	ADS43323	Ads43323 Bacterial
733	7	2.5	361	8	ABM80632	Abm80632 Tumour-as	806	7	2.5	491	4	ABBS8307	Abbs8307 Drosophil
734	7	2.5	364	6	ABP70443	Abp70443 Amino aci	807	7	2.5	491	4	ABBG7058	Abbg7058 Drosophil
735	7	2.5	364	6	ABP70442	Abp70442 Amino aci	808	7	2.5	491	7	ADK11397	Adk11397 Drosophil
736	7	2.5	364	6	ABJ37502	Abj37502 HCV relat	809	7	2.5	491	7	ADK11399	Adk11399 Drosophil
737	7	2.5	365	6	ABP70440	Abp70440 Amino aci	810	7	2.5	491	8	ADS96582	Ads96582 Drosophil
738	7	2.5	366	4	ABB61562	Abb61562 Drosophil	811	7	2.5	492	8	ADN20281	Adn20281 Bacterial
739	7	2.5	368	8	ADL35838	Adl35838 Human sin	812	7	2.5	493	8	ADS24658	Ads24658 Bacterial
740	7	2.5	368	8	ABM80095	Abm80095 Tumour-as	813	7	2.5	495	8	ADS30904	Ads30904 Bacterial
741	7	2.5	368	8	ADN25990	Adn25990 Bacterial	814	7	2.5	498	8	ADS28858	Ads28858 Bacterial
742	7	2.5	370	2	AAAR29528	Aar29528 HCV antig	815	7	2.5	499	5	ABP26573	Abp26573 Streptoco
743	7	2.5	370	3	AAAY74818	Aay74818 Neisseria	816	7	2.5	504	5	ABP63086	Abp63086 FLO11 gen
744	7	2.5	370	3	AAAY74819	Aay74819 Neisseria	817	7	2.5	505	7	ABO65745	Abu65745 Klebsiell
745	7	2.5	370	3	AAAY74820	Aay74820 Neisseria	818	7	2.5	513	4	AAAB69032	Aab69032 HCV recom
746	7	2.5	370	6	ABU16755	Abu16755 Protein e	819	7	2.5	513	5	ABP30089	Abp30089 Streptoco
747	7	2.5	370	8	ADO5010	Ado5010 M. catarr	820	7	2.5	513	6	ABU01157	Abu01157 S. pneumo
748	7	2.5	370	8	ADO80311	Ado80311 Xylella s	821	7	2.5	513	6	ABP81364	Abp81364 Streptoco
749	7	2.5	370	8	ADO80309	Ado80309 Xylella s	822	7	2.5	513	7	ABW01897	Abw01897 HCV CKS-3
750	7	2.5	371	8	ADN26632	Adn26632 Bacterial	823	7	2.5	513	8	ADK46256	Adk46256 Streptoco
751	7	2.5	371	8	ADN26874	Adn26874 Bacterial	824	7	2.5	513	8	ADS42400	Ads42400 Bacterial
752	7	2.5	372	2	AAAW56626	Aaw56626 Staphyloc	825	7	2.5	518	6	ABW70162	Abw70162 Photornab
753	7	2.5	372	6	ADA34389	Ada34389 Acinetoba	826	7	2.5	518	8	ADQ76691	Adq76691 Human KIM
754	7	2.5	374	7	ADI23989	Adi23989 Construct	827	7	2.5	519	8	ADS41654	Ads41654 Bacterial
755	7	2.5	377	6	ABJ18505	Abj18505 Human Cry	828	7	2.5	521	4	AAAB78945	Aab78945 C. glutam

829	7	2.5	522	3	AAG49803	Rag49803 Arabidops	902	7	2.5	582	8	ADS42666	Ads42666 Bacterial
830	7	2.5	522	8	ADN5829	Adn25829 Bacterial	903	7	2.5	582	8	ADN18131	Adn18131 Bacterial
831	7	2.5	524	5	AAE13099	Aae13099 Staphyloc	904	7	2.5	583	8	ADS42479	Ads42479 Bacterial
832	7	2.5	524	8	ADS45022	Ads45022 Bacterial	905	7	2.5	585	2	NAR58589	Nar58589 Hepatitis
833	7	2.5	526	4	ABG28548	Abg28548 Novel hum	906	7	2.5	585	4	ABG24297	Abg24297 Novel hum
834	7	2.5	528	6	ABM69162	Abm69162 Photorhab	907	7	2.5	585	6	AAE37951	Aae37951 Pseudomon
835	7	2.5	528	7	ADH44162	Adh44162 Hepatitis	908	7	2.5	585	8	ADL17780	Adl17780 Hepatitis
836	7	2.5	528	8	ADN37289	Adn37289 Barley st	909	7	2.5	585	8	ADS23862	Ads23862 Bacterial
837	7	2.5	529	7	ADB70185	Adb70185 C. neofor	910	7	2.5	587	4	AAU35367	Aau35367 Haemophil
838	7	2.5	529	8	ADS21119	Ads21119 Bacterial	911	7	2.5	587	4	AAE88504	Aae88504 Haemophil
839	7	2.5	530	6	ABU21280	Abu21280 Protein e	912	7	2.5	587	5	AAU91435	Aau91435 Haemophil
840	7	2.5	530	6	ABU22304	Abu22304 Protein e	913	7	2.5	587	6	ABU301139	Abu301139 Bacterial
841	7	2.5	533	4	AAU35783	Aau35783 Helicobac	914	7	2.5	589	8	ADS29831	Ads29831 Bacterial
842	7	2.5	533	6	ABU30893	Abu30893 Protein e	915	7	2.5	590	6	ABM70726	Abm70726 Photorhab
843	7	2.5	537	8	ADS22392	Ads22392 Bacterial	916	7	2.5	590	8	ADN18082	Adn18082 Bacterial
844	7	2.5	539	8	ADN25209	Adn25209 Bacterial	917	7	2.5	591	8	ADF70703	Adf70703 Acetic-ac
845	7	2.5	545	6	ABU23013	Abu23013 Protein e	918	7	2.5	592	8	ADN25035	Adn25035 Bacterial
846	7	2.5	546	7	ADC94354	Adc94354 E. faeciu	919	7	2.5	593	7	ADF05083	Adf05083 Bacterial
847	7	2.5	547	4	AAE79015	Aae79015 C. glutami	920	7	2.5	593	8	ADN20003	Adn20003 Bacterial
848	7	2.5	547	4	AAG90928	Aag90928 C. glutami	921	7	2.5	594	4	AAU57050	Aau57050 Propionib
849	7	2.5	547	7	ABR63524	Abf63524 C. glutami	922	7	2.5	594	6	ABM53569	Abm53569 Propionib
850	7	2.5	547	7	ADL65547	Adl65547 C. glutami	923	7	2.5	594	6	ABM73376	Abm73376 Staphyloc
851	7	2.5	548	7	ADC97000	Adc97000 E. faeciu	924	7	2.5	594	7	ADC97623	Adc97623 E. faeciu
852	7	2.5	549	7	ADC73281	Adc73281 Escherich	925	7	2.5	595	7	ABG75195	Abg75195 M. licheni
853	7	2.5	549	8	ADS25614	Ads25614 Bacterial	926	7	2.5	598	4	AAU65295	Aau65295 Propionib
854	7	2.5	554	2	AAE50077	Aae50077 NANBH vir	927	7	2.5	598	5	ABM61814	Abm61814 Propionib
855	7	2.5	554	2	AAW48661	Aaw48661 RG fusion	928	7	2.5	598	6	ABM61814	Abm61814 Propionib
856	7	2.5	554	4	AAG90339	Aag90339 C. glutami	929	7	2.5	598	8	ADN22808	Adn22808 Bacterial
857	7	2.5	554	8	ADJ81682	Adj81682 Non-A-non	930	7	2.5	599	8	ADN28276	Adn28276 Bacterial
858	7	2.5	554	8	ADM94400	Adm94400 Soybean M	931	7	2.5	601	8	ADN22277	Adn22277 Bacterial
859	7	2.5	555	6	ABU19827	Abu19827 Protein e	932	7	2.5	602	5	ABU23460	Abu23460 Protein e
860	7	2.5	555	7	ADC73279	Adc73279 Escherich	933	7	2.5	604	6	ABM48305	Abm48305 Listeria
861	7	2.5	556	8	ADS29774	Ads29774 Bacterial	934	7	2.5	607	5	ABP62771	Abp62771 Protein f
862	7	2.5	558	2	AAW48662	Aaw48662 GR fusion	935	7	2.5	607	6	ABP58190	Abp58190 Luciferas
863	7	2.5	558	4	AAG06559	Ag06559 Novel hum	936	7	2.5	607	7	ADJ72182	Adj72182 Streptomy
864	7	2.5	558	5	ABP27849	Abp27849 Streptoco	937	7	2.5	608	8	ADF70705	Adf70705 Acetic-ac
865	7	2.5	559	6	ABU21221	Abu21221 Protein e	938	7	2.5	609	2	AAE51170	Aae51170 Hepatitis
866	7	2.5	560	6	ABU00845	Abu00845 S. pneumo	939	7	2.5	612	8	ADS29013	Ads29013 Bacterial
867	7	2.5	560	6	ABP81330	Abp81330 Streptoco	940	7	2.5	613	4	AAU04887	Aau04887 Micromono
868	7	2.5	560	8	ADS30310	Ads30310 Bacterial	941	7	2.5	613	5	AAE19893	Aae19893 Hepatitis
869	7	2.5	564	6	ABU40586	Abu40586 Protein e	942	7	2.5	613	6	ABU28306	Abu28306 Protein e
870	7	2.5	566	8	ADH39713	Adh39713 Streptomy	943	7	2.5	613	7	ABW00344	Abw00344 Hepatitis
871	7	2.5	568	5	ABP27905	Abp27905 Streptoco	944	7	2.5	613	8	ADS23090	Ads23090 Bacterial
872	7	2.5	568	6	ABU46439	Abu46439 Protein e	945	7	2.5	614	6	ABM66127	Abm66127 Propionib
873	7	2.5	570	6	ABM72766	Abm72766 Staphyloc	946	7	2.5	615	2	AAW37807	Aaw37807 Nonstruct
874	7	2.5	571	6	ABU49048	Abu49048 Protein e	947	7	2.5	621	6	ABU20490	Abu20490 Protein e
875	7	2.5	572	8	ADS26086	Ads26086 Bacterial	948	7	2.5	621	8	ADS21702	Ads21702 Pseudomon
876	7	2.5	573	5	ABP28687	Abp28687 Streptoco	949	7	2.5	623	7	ABO82427	Abo82427 Alloiooc
877	7	2.5	573	5	ABB48813	Abb48813 Listeria	950	7	2.5	625	6	ADB09723	Adb09723 Alloiooc
878	7	2.5	574	6	ADB11648	Adb11648 Alloiooc	951	7	2.5	625	6	ADS23228	Ads23228 Bacterial
879	7	2.5	575	4	ABB47263	Abb47263 Enterococ	952	7	2.5	628	2	AAW85701	Aaw85701 Pinene sy
880	7	2.5	575	6	ABU11393	Abu11393 Protein e	953	7	2.5	628	3	AAI90837	Aai90837 Grand fir
881	7	2.5	575	6	ABM72335	Abm72335 Staphyloc	954	7	2.5	628	4	AAE69371	Aae69371 Grand fir
882	7	2.5	575	7	ADH87501	Adh87501 Enterococ	955	7	2.5	630	2	ADN33110	Adn33110 Hepatitis
883	7	2.5	577	8	ADN20264	Adn20264 Bacterial	956	7	2.5	631	2	AAE82854	Aae82854 NS3 serin
884	7	2.5	577	8	ADN20361	Adn20361 Bacterial	957	7	2.5	631	2	AAE82854	Aae82854 NS3 serin
885	7	2.5	579	8	ADS21357	Ads21357 Bacterial	958	7	2.5	631	2	AAW31884	Aaw31884 A nonstru
886	7	2.5	580	5	ABP40766	Abp40766 Staphyloc	959	7	2.5	631	2	AAW26160	Aaw26160 Serine pr
887	7	2.5	580	8	ADS08083	Ads08083 Staphyloc	960	7	2.5	631	2	AAW93482	Aaw93482 HCV NS3 p
888	7	2.5	581	8	ADS30307	Ads30307 Bacterial	961	7	2.5	631	2	AAI14354	Aai14354 Hepatitis
889	7	2.5	581	8	ADN17801	Adn17801 Bacterial	962	7	2.5	631	2	AAI15806	Aai15806 HCV strai
890	7	2.5	581	8	ADN27071	Adn27071 Bacterial	963	7	2.5	631	3	AAE41972	Aae41972 Human ORF
891	7	2.5	582	4	AAU38413	Aau38413 Salmonell	964	7	2.5	631	3	AAE118158	Aae118158 Hepatitis
892	7	2.5	582	4	AAU34522	Aau34522 E. coli c	965	7	2.5	632	5	AAE21847	Aae21847 Hepatitis
893	7	2.5	582	6	ABU49428	Abu49428 Protein e	966	7	2.5	632	5	AAE19905	Aae19905 Hepatitis
894	7	2.5	582	6	ABU48048	Abu48048 Proteine	967	7	2.5	632	6	ABU23866	Abu23866 Protein e
895	7	2.5	582	6	ABU31837	Abu31837 Protein e	968	7	2.5	632	6	ABW00356	Abw00356 Hepatitis
896	7	2.5	582	6	ABU45164	Abu45164 Protein e	969	7	2.5	632	8	ADG47669	Adg47669 HCV NS3/4
897	7	2.5	582	6	ABU50086	Abu50086 Protein e	970	7	2.5	632	8	ADO36213	Ado36213 Hepatitis
898	7	2.5	582	6	ABU47313	Abu47313 Protein e	971	7	2.5	632	8	ADO79387	Ado79387 Hepatitis
899	7	2.5	582	6	ABU28578	Abu28578 Protein e	972	7	2.5	633	3	AAI81755	Aai81755 Streptoco
900	7	2.5	582	6	ABU39189	Abu39189 Protein e	973	7	2.5	633	4	AAU37725	Aau37725 Streptoco
901	7	2.5	582	7	ABO65563	Ab065563 Klebsiell	974	7	2.5	633	4	AAU37725	Aau37725 Streptoco

975 7 2.5 633 6 ABU01533 S. pneumo
976 7 2.5 633 6 ABU46048 Protein e
977 7 2.5 633 8 ADK47288 Streptoco
978 7 2.5 634 6 AD809721 Alloiooc
979 7 2.5 635 5 ABP27552 Streptoco
980 7 2.5 635 5 AB54378 Lactococ
981 7 2.5 635 6 ABU46609 Protein e
982 7 2.5 635 6 AB42556 Novobioc
983 7 2.5 635 8 ADS29366 Bacterial
984 7 2.5 636 5 ABP30300 Streptoco
985 7 2.5 636 6 ABU41603 Protein e
986 7 2.5 637 6 ABM69282 Photorhab
987 7 2.5 637 6 ABU44191 Protein e
988 7 2.5 638 4 AAE10068 Hepatitis
989 7 2.5 639 6 ABU49363 Protein e
990 7 2.5 642 6 ABU24552 Protein e
991 7 2.5 644 5 ABP27551 Streptoco
992 7 2.5 645 6 ABU21789 Protein e
993 7 2.5 645 8 ADS23263 Bacterial
994 7 2.5 646 2 AAY17894 HCV NS4A-
995 7 2.5 646 2 AAY17892 HCV NS4A-
996 7 2.5 646 2 AAY24950 HCV NS4A-
997 7 2.5 647 8 Adn22057 Bacterial
998 7 2.5 647 8 Adn24816 Bacterial
999 7 2.5 649 2 AAR14546 hSOD-HCV
1000 7 2.5 649 6 ABU19934 Protein e

ALIGNMENTS

RESULT 1
AAy81709
ID AAY81709 standard; protein; 279 AA.
XX
AC AAY81709;
XX
DT 02-JUN-2000 (first entry)
XX
DE Streptococcus pneumoniae protein sequence ID2.
XX
KW Streptococcus pneumoniae infection; immunogen; antigen; diagnosis; AIDS;
KW bacterial pneumonia; asplenia; heart disease; lung disease; alcoholism;
KW kidney disease; diabetes; immunosuppressive disorder; otitis media;
KW pneumococcal septicaemia; sinusitis; meningitis; therapy.
XX
OS Streptococcus pneumoniae.
XX
FN WO200006738-A2.
XX
PD 10-FEB-2000.
XX
PD 27-JUL-1999; 99WO-GB002452.
XX
PR 27-JUL-1998; 98GB-00016336.
PR 19-MAR-1999; 99US-0125329P.
XX
PA (MICR-) MICROBIAL TECHNIQS LTD.
XX
XX Le Page RWF, Wells JM, Hanniffy SB, Hanebro PM;
XX WPI; 2000-195301/17.
DR N-PSDB; AAZ91805.
XX
PT Streptococcal proteins and polynucleotides useful for diagnosis,
PT treatment and prophylaxis of bacterial infections.
XX
PS Claim 2; Page 40; 76pp; English.
XX
XX This sequence represents a Streptococcus pneumoniae protein of the
CC invention. The proteins (or their homologues, derivatives and/or
CC fragments) are useful as immunogens or antigens. Immunogenic or antigenic
CC compositions comprising the proteins are useful as vaccines and also in

CC diagnostic assays. The sequences are useful for the detection or
CC diagnosis of S. pneumoniae infection, by contacting a sample to be tested
CC with them. Agents capable of antagonising, inhibiting or interfering with
CC the function or expression of the protein or polypeptide are useful in
CC medical compositions in the treatment or prophylaxis of S. pneumoniae
CC infection. As the sequences can be used to treat S. pneumoniae infection,
CC they can be used to treat bacterial pneumonia, which has high rates in
CC young children, the elderly, and in patients with predisposing conditions
CC such as asplenia, heart, lung and kidney disease, diabetes, alcoholism,
CC or with immunosuppressive disorders, especially AIDS. They can also be
CC used to treat pneumococcal septicaemia, otitis media, sinusitis, and
CC meningitis
XX
SQ Sequence 279 AA;
Query Match 100.0%; Score 279; DB 3; Length 279;
Best Local Similarity 100.0%; Pred. No. 7.7e-263;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIALENNVFTYQEGTTPLASAALSDVSLTIEDGSYTALIGHTSGKSTILQLLGLVPS 60
DB 1 MGIALENNVFTYQEGTTPLASAALSDVSLTIEDGSYTALIGHTSGKSTILQLLGLVPS 60
QY 61 QGSVRVFDLTITSTSKNDIRIQKQVGLVFOFAENQIFETVLDKDAFGPQNFVSEED 120
DB 61 QGSVRVFDLTITSTSKNDIRIQKQVGLVFOFAENQIFETVLDKDAFGPQNFVSEED 120
QY 121 AVKTAREKLALVGIDESLFDSPFELSGGOMRRVAJAGILAMEPAILVLDEPTAGLDPLG 180
DB 121 AVKTAREKLALVGIDESLFDSPFELSGGOMRRVAJAGILAMEPAILVLDEPTAGLDPLG 180
QY 181 RKELMTLPFKLHQSGMTIVLVTHLMDDDVAEYANQVYVMEKRLVKGKPSDVQDVVFME 240
DB 181 RKELMTLPFKLHQSGMTIVLVTHLMDDDVAEYANQVYVMEKRLVKGKPSDVQDVVFME 240
QY 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEEFKESLNG 279
DB 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEEFKESLNG 279
RESULT 2
ABU02751
ID ABU02751 standard; protein; 279 AA.
XX
AC ABU02751;
XX
DT 23-OCT-2003 (revised)
DT 11-FEB-2003 (first entry)
XX
DE S. pneumoniae type 4 strain protein from coding region #2330.
XX
KW Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection;
KW antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;
KW gene therapy; vaccine.
XX
OS Streptococcus pneumoniae; type 4 strain.
XX
FN WO200277021-A2.
XX
PD 03-OCT-2002.
XX
PD 27-MAR-2002; 2002WO-IB002163.
XX
PR 27-MAR-2001; 2001GB-00007658.
XX
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX
PI Masignani V, Tettelin H, Fraser C;
DR WPI; 2003-040579/03.
DR N-PSDB; ABX08042.
XX

PT New proteins and nucleic acid molecules from Streptococcus pneumoniae,
 PT useful as medicaments for treating or preventing a disease or infection
 PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
 PT ear infection.

XX Claim 1; SEQ ID NO 4660; 56pp; English.

XX The invention relates to a protein comprising or having at least 50%
 CC identity to any of the 2469 amino acid sequences, identified in the
 CC specification (available on a computer readable format), or its fragment,
 CC expressed from 2469 of 2489 identified DNA coding regions from the
 CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as
 CC ABS56454. Also included are an antibody which binds one of the proteins,
 CC treating a patient by administering the protein, DNA or antibody (in a
 CC composition), a kit comprising first and second primers, which are the
 CC nucleic acid cited above or fragments between nucleotides 8-100 of a
 CC sequence not defined in the specification, for amplifying a target
 CC sequence contained within a Streptococcus nucleic acid sequence, where
 CC the first primer is substantially complementary to the target sequence
 CC and the second primer is substantially complementary to the complement of
 CC the target sequence, and where the parts of the primers having
 CC substantial complementarity define the termini of the target sequence to
 CC be amplified, assay comprising contacting a test compound with the
 CC protein, and determining whether the test compound binds to the protein
 CC and a Streptococcus pneumoniae bacterium, where one or more genes
 CC encoding the proteins has been rendered inactive. The proteins, nucleic
 CC acid molecules, antibody and compositions are useful as medicaments for
 CC treating or preventing a disease or infection due to streptococcus
 CC bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis
 CC media or ear infection. They are also useful in developing vaccines,
 CC diagnostics and antibiotics. The methods are useful for identifying
 CC immunodominant proteins. The present sequence is one of the 2469 proteins
 CC expressed by the identified coding regions from the genomic sequence.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to
 CC standardise OS field)

XX SQ Sequence 279 AA;

Query Match 100.0%; Score 279; DB 6; Length 279;
 Best Local Similarity 100.0%; Pred. No. 7.7e-263;
 Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGIALENNFTYQSGTPLASALSDVSLTIEDGVSYALIGHTGSGKSTILQLNGLLVPS 60
 Db 1 MGIALENNFTYQSGTPLASALSDVSLTIEDGVSYALIGHTGSGKSTILQLNGLLVPS 60
 Qy 61 QGSVRVFDTLTSTSKNKDIRQIRKQVGLVFPQFAENQIFETVLKDVAFQPNFGVSEED 120
 Db 61 QGSVRVFDTLTSTSKNKDIRQIRKQVGLVFPQFAENQIFETVLKDVAFQPNFGVSEED 120
 Qy 121 AVKTAREKIALVGDIESLFDSPPELSCGQRRVAIAGILAMEPAAILVLDPTAGLDPLG 180
 Db 121 AVKTAREKIALVGDIESLFDSPPELSCGQRRVAIAGILAMEPAAILVLDPTAGLDPLG 180
 Qy 181 RKELMTLPKLLHQSGMTIVLVTHLMDVDAEYANQVYVMEKRLVKGGKPSDVFDQVWME 240
 Db 181 RKELMTLPKLLHQSGMTIVLVTHLMDVDAEYANQVYVMEKRLVKGGKPSDVFDQVWME 240
 Qy 241 EVQLGVPKITAFCKRLADRGVSFKELPIKIEPKESLNG 279
 Db 241 EVQLGVPKITAFCKRLADRGVSFKELPIKIEPKESLNG 279

RESULT 3
 AAM01016
 ID AAM01016 standard; protein; 279 AA.

XX AAM01016;
 AC
 XX
 DT 02-OCT-2001 (first entry)
 XX

DE CFE 15 protein sequence.
 XX Antibacterial; vaccine; gene therapy; bacterial cell wall viability; CFE;
 KW CEG; Conserved Essential Gene; bacterial infection; antisense therapy;
 KW antibiotic resistance.

XX Streptococcus pneumoniae.

OS W0200149721-A2.

PN 12-JUL-2001.

PD 29-DEC-2000; 2000WO-US035604.

PF 30-DEC-1999; 99US-0174089P.

PR (BRIM) BRISTOL-MYERS SQUIBB CO.

PA Dougherty TV, Pucci MJ, Dougherty BA, Davison DB, Bruccoleri RE;
 PI Thanassi JA;

PI WPI; 2001-496721/54.

PI N-PSDB; AAH90715.

XX Nucleic acids encoding conserved essential genes involved in bacterial
 PT replication which are potential targets for the treatment of antibiotic
 PT resistant bacterial infections.

XX Claim 27; Page 254-255; 380pp; English.

XX The present invention relates to nucleic acids (AAH90701-AAH90918)
 CC encoding polypeptides (AAM01002-AAM01114), which are essential for the
 CC viability of a bacterial cell wall. The acronym CFE stands for "CEG For
 CC Expression", where CEG stands for "Conserved Essential Gene". The nucleic
 CC acids are useful for detecting the presence of proteins essential for the
 CC viability of a bacterial cell wall in samples such as cells, tissues,
 CC biological fluids, blood, serum, nose, ear or throat swabs with ligands,
 CC and for detecting corresponding target nucleic acid molecules with
 CC complementary sequences. The nucleic acids are also useful for
 CC determining whether a genomic nucleotide sequence of interest is
 CC essential for viability of a bacterial cell or whether it resides within
 CC an operon, by integrating an exogenous nucleotide sequence comprising a
 CC portion of an open reading frame of the genomic sequence of interest
 CC (comprising 200-500 base pairs) into the genomic sequence of interest
 CC which confers a selectable phenotype to the cell, and determining cell
 CC viability with a selection agent such as chloramphenicol. The nucleic
 CC acids and proteins are also useful as vaccines and for treating bacterial
 CC infections with gene therapy and antisense therapy. The nucleic acids
 CC also enable identification of targets suitable for the treatment of
 CC antibiotic resistant bacterial infections

XX SQ Sequence 279 AA;

Query Match 95.7%; Score 267; DB 4; Length 279;
 Best Local Similarity 100.0%; Pred. No. 3.7e-251;
 Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGIALENNFTYQSGTPLASALSDVSLTIEDGVSYALIGHTGSGKSTILQLNGLLVPS 60
 Db 1 MGIALENNFTYQSGTPLASALSDVSLTIEDGVSYALIGHTGSGKSTILQLNGLLVPS 60
 Qy 61 QGSVRVFDTLTSTSKNKDIRQIRKQVGLVFPQFAENQIFETVLKDVAFQPNFGVSEED 120
 Db 61 QGSVRVFDTLTSTSKNKDIRQIRKQVGLVFPQFAENQIFETVLKDVAFQPNFGVSEED 120
 Qy 121 AVKTAREKIALVGDIESLFDSPPELSCGQRRVAIAGILAMEPAAILVLDPTAGLDPLG 180
 Db 121 AVKTAREKIALVGDIESLFDSPPELSCGQRRVAIAGILAMEPAAILVLDPTAGLDPLG 180
 Qy 181 RKELMTLPKLLHQSGMTIVLVTHLMDVDAEYANQVYVMEKRLVKGGKPSDVFDQVWME 240
 Db 181 RKELMTLPKLLHQSGMTIVLVTHLMDVDAEYANQVYVMEKRLVKGGKPSDVFDQVWME 240

QY 241 EVOLGVPKITAFCCKRLADRGVSFKRLP 267
 DB 241 EVOLGVPKITAFCCKRLADRGVSFKRLP 267

RESULT 4
 ADK47865
 ID ADK47865 standard; protein; 279 AA.
 AC ADK47865;
 DT 20-MAY-2004 (first entry)
 DE Streptococcus pneumoniae protein, Seq ID No 4380.
 XX Antibacterial; Gene therapy; Vaccine; Streptococcus pneumoniae.
 KW Streptococcus pneumoniae.
 OS US6699703-B1.
 PN 02-MAR-2004.
 PD 26-MAY-2000; 2000US-00583110.
 PF 02-JUL-1997; 97US-0051553P.
 PR 12-MAY-1998; 98US-0085131P.
 PR 30-JUN-1998; 98US-00107433.
 XX (GENO-) GENOME THERAPEUTICS CORP.
 PA Doucette-Stamm L, Bush D, Zeng Q, Opperman T, Houseweart CE;
 PI WPI: 2004-212399/20.
 XX N-PSDB; ADK45204.
 DR New nucleic acid molecules and polypeptides useful for diagnosing,
 PT preventing and treating pathological conditions resulting from bacterial
 PT infection, e.g. Streptococcus pneumoniae infection, and in drug
 PT screening.
 XX Disclosure; SEQ ID NO 4380; 301pp; English.
 PS The invention relates to isolated Streptococcus pneumoniae nucleic acids
 XX and polypeptides. The nucleic acids and proteins are useful for
 CC diagnosing, preventing and treating pathological conditions resulting
 CC from bacterial infection, such as S. pneumoniae infection. These may also
 CC be used for drug screening procedures. The present sequence represents a
 CC Streptococcus pneumoniae polypeptide of the invention. Note: The sequence
 CC data for this patent did not appear in the printed specification but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html.
 XX Sequence 279 AA;
 SQ Query Match 95.7%; Score 267; DB 8; Length 279;
 Best Local Similarity 100.0%; Pred. No. 3.7e-251;
 Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTALENNVNTYQGTPLASAAALSDVSLTIEDSGSYTALIGHTSGKSTILQLLGLLVPS 60
 DB 1 MGTALENNVNTYQGTPLASAAALSDVSLTIEDSGSYTALIGHTSGKSTILQLLGLLVPS 60

QY 61 QGSVRVFDTLITSTSKNKDRIQRKQVGLVQFAENQIFETVLKDVAFQPGFVSEED 120
 DB 61 QGSVRVFDTLITSTSKNKDRIQRKQVGLVQFAENQIFETVLKDVAFQPGFVSEED 120

QY 121 AVKTAREKIALVGLIDESLFRSPPELGGQRRVVAIAGILAMEPAIILVDEPTAGLDPLG 180
 DB 121 AVKTAREKIALVGLIDESLFRSPPELGGQRRVVAIAGILAMEPAIILVDEPTAGLDPLG 180

QY 181 RKEIMTLFKKLHOSGMTIVLTHLDDVAEYANQVYVMEKRLVKGKPSDFQDVVFME 240
 DB 181 RKEIMTLFKKLHOSGMTIVLTHLDDVAEYANQVYVMEKRLVKGKPSDFQDVVFME 240

Db 181 RKEIMTLFKKLHOSGMTIVLTHLDDVAEYANQVYVMEKRLVKGKPSDFQDVVFME 240
 QY 241 EVOLGVPKITAFCCKRLADRGVSFKRLP 267
 DB 241 EVOLGVPKITAFCCKRLADRGVSFKRLP 267

RESULT 5
 ADR96203
 ID ADR96203 standard; protein; 280 AA.
 AC ADR96203;
 DT 16-DEC-2004 (first entry)
 DE Novel S. pneumoniae protein sequence, SEQ ID 4838.
 XX Meningitis; bacteraemia; pneumonia; otitis media; vaccine;
 KW bacterial infection.
 OS Streptococcus pneumoniae.
 PN US6800744-B1.
 PD 05-OCT-2004.
 PF 30-JUN-1998; 98US-00107433.
 PR 02-JUL-1997; 97US-0051553P.
 PR 12-MAY-1998; 98US-0085131P.
 XX (GENO-) GENOME THERAPEUTICS CORP.
 PA Doucette-Stamm LA, Bush D;
 PI WPI: 2004-697205/68.
 XX N-PSDB; ADR93600.
 DR New isolated nucleic acid encoding a Streptococcus pneumoniae
 PT polypeptide, useful for diagnosing, preventing and/or treating
 PT pathological conditions resulting from the bacterial infection.
 XX Disclosure; SEQ ID NO 4838; 151pp; English.
 PS The invention relates to an isolated nucleic acid comprising a sequence
 XX encoding a Streptococcus pneumoniae ADR9366polypeptide, or its
 CC fragments, with any of 9 fully defined sequences (appearing as ADR94308,
 CC ADR94489, ADR94800, ADR94837, ADR94969, ADR95253, ADR95642, ADR95682,
 CC ADR96079) or any of the fully defined sequences appearing as ADR91705,
 CC ADR91886, ADR92197, ADR92234, ADR93039, ADR93079, ADR92366, ADR92650 or
 CC ADR93476 or at least 20 or 30 consecutive nucleotides of the nucleotide
 CC sequences, or at least 40, 60 or 300 consecutive nucleotides, which is
 CC hybridisable under high stringency conditions to the nucleotide sequence.
 CC The nucleic acids and proteins are chosen from 5206 disclosed sequences.
 CC Also included are a recombinant expression vector comprising the isolated
 CC nucleic acid cited above operably linked to a transcription regulatory
 CC element, a cell comprising the recombinant expression vector and a probe
 CC comprising at least 20 consecutive nucleotides of the nucleotide
 CC sequences as cited above. The methods and compositions of the present
 CC invention are useful for the diagnosis, prevention and/or treatment of
 CC pathological conditions resulting from bacterial infection by
 CC Streptococcus pneumoniae e.g. pneumonia, bacteraemia, meningitis and
 CC otitis media. The present sequence is one of the 2603 disclosed S.
 CC pneumoniae protein sequences. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=6800744B1.
 XX Sequence 280 AA;
 SQ Query Match 95.7%; Score 267; DB 8; Length 280;
 Best Local Similarity 100.0%; Pred. No. 3.8e-251;
 Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC fcp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 279 AA;

Query Match 59.9%; Score 167; DB 4; Length 279;
Best Local Similarity 99.6%; Pred. No. 9e-154;
Matches 267; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 YQSGTPLASALSDVSLTIEDGTYTALIGHTSGKSTILQLLNGLLVPSQSVRVFTLI 71
DB 12 YQSGTPLASALSDVSLTIEDGTYTALIGHTSGKSTILQLLNGLLVPSQSVRVFTLI 71
QY 72 TSTSKNKDIRQIRKQVGLVFPQFAENQIFETVLKDVAFQPNFGVSEDAVKTAREKAL 131
DB 72 TSTSKNKDIRQIRKQVGLVFPQFAENQIFETVLKDVAFQPNFGVSEDAVKTAREKAL 131
QY 132 VGIDESLFDSPPELGGQMRVAIAGILAMEPAILVLDDEPTAGLDPLGRKELMTLPK 191
DB 132 VGIDESLFDSPPELGGQMRVAIAGILAMEPAILVLDDEPTAGLDPLGRKELMTLPK 191
QY 192 HQSGMTIVLTHLMDVDAEYANQVYVMEKGRVKGKPSDFQDVFMEEVQLGVPKITA 251
DB 192 HQSGMTIVLTHLMDVDAEYANQVYVMEKGRVKGKPSDFQDVFMEEVQLGVPKITA 251
QY 252 FCRLADRGVSFKRLPIKIEEFKESLNG 279
DB 252 FCRLADRGVSFKRLPIKIEEFKESLNG 279

RESULT 7
ABU46314
ID ABU46314 standard; protein; 279 AA.
XX
AC ABU46314;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #31841.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Streptococcus pneumoniae.
XX FN WO200277183-A2.
XX
XX PD 03-OCT-2002.
XX
XX PF 21-MAR-2002; 2002WO-US009107.
XX
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
XX DR N-PSDB; ACAS0184.
XX
XX PT New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to

QY 1 MGTALENVNTYQEGTPLASALSDVSLTIEDGTYTALIGHTSGKSTILQLLNGLLVPS 60
DB 2 MGTALENVNTYQEGTPLASALSDVSLTIEDGTYTALIGHTSGKSTILQLLNGLLVPS 61
QY 61 QGSRVFPDTLITSTSKNKDIRQIRKQVGLVFPQFAENQIFETVLKDVAFQPNFGVSEED 120
DB 62 QGSRVFPDTLITSTSKNKDIRQIRKQVGLVFPQFAENQIFETVLKDVAFQPNFGVSEED 121
QY 121 AVKTAREKALVGLIDESLFDSPPELGGQMRVAIAGILAMEPAILVLDDEPTAGLDPLG 180
DB 122 AVKTAREKALVGLIDESLFDSPPELGGQMRVAIAGILAMEPAILVLDDEPTAGLDPLG 181
QY 181 RKELMTLPFKLHQSGMTIVLTHLMDVDAEYANQVYVMEKGRVKGKPSDFQDVFMEE 240
DB 182 RKELMTLPFKLHQSGMTIVLTHLMDVDAEYANQVYVMEKGRVKGKPSDFQDVFMEE 241
QY 241 EVQLGVPKITAFAFCRLADRGVSFKRLP 267
DB 242 EVQLGVPKITAFAFCRLADRGVSFKRLP 268

RESULT 6
AAU37847
ID AAU37847 standard; protein; 279 AA.
XX
AC AAU37847;
XX
DT 14-FEB-2002 (first entry)
XX
DE Streptococcus pneumoniae cellular proliferation protein #276.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
XX
XX OS Streptococcus pneumoniae.
XX
XX FN WO200170955-A2.
XX
XX PD 27-SEP-2001.
XX
XX PF 21-MAR-2001; 2001WO-US009180.
XX
XX PR 21-MAR-2000; 2000US-0191078P.
XX PR 23-MAY-2000; 2000US-0206848P.
XX PR 26-MAY-2000; 2000US-0207727P.
XX PR 23-OCT-2000; 2000US-0242578P.
XX PR 27-NOV-2000; 2000US-0253625P.
XX PR 22-DEC-2000; 2000US-0257931P.
XX PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
XX DR N-PSDB; AAS55706.
XX
XX PT New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 13440; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the genes,
XX their use in the discovery of novel antibiotics, the essential genes
XX themselves and the encoded proteins. The prokaryotes used are Escherichia
XX coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX useful for the identification of potential new targets for antibiotic
XX development. The antisense nucleic acids can also be used to identify
XX proteins used in proliferation, to express these proteins, and to obtain

PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 74238; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 279 AA;

Query Match 59.9%; Score 167; DB 6; Length 279;
Best Local Similarity 99.6%; Pred. No. 9e-154;
Matches 267; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 YQSGTPLASALSDVSLTIEDGYSYTLIGHTGSGKSTILOLNLGLVPSQGSVRVPTLI 71
DB 12 YQSGTPLASALSDVSLTIEDGYSYTLIGHTGSGKSTILOLNLGLVPSQGSVRVPTLI 71

QY 72 TSTSNNKDIQIRKQVGLVFQFAENQIFETVLKDVAFGQNFQVSEEDAVKTAREKIAL 131
DB 72 TSTSNNKDIQIRKQVGLVFQFAENQIFETVLKDVAFGQNFQVSEEDAVKTAREKIAL 131

QY 132 VGIDESLFDSPPELSCGQMRRAIAGILAMEPAILVLDEPTAGLDPLGRKELMTLPKKL 191
DB 132 VGIDESLFDSPPELSCGQMRRAIAGILAMEPSILVLDEPTAGLDPLGRKELMTLPKKL 191

QY 192 HQSGMTIVLTHLMDDVAEYANQVYVMEKGRVKGKPSDFQDVPMEEVQLGVPKITA 251
DB 192 HQSGMTIVLTHLMDDVAEYANQVYVMEKGRVKGKPSDFQDVPMEEVQLGVPKITA 251

QY 252 FCRLADRGVSFKRLPIKIEFKESLNG 279
DB 252 FCRLADRGVSFKRLPIKIEFKESLNG 279

RESULT 8
ABBS3584
ID ABB53584 standard; protein; 288 AA.
XX
AC ABB53584;
XX
DT 29-AUG-2003 (revised)
DT 16-MAY-2002 (first entry)
XX
XX Lactococcus lactis protein ychE.

XX Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
XX Lactococcus lactis; IL1403.
OS
PN PR2807446-A1.
XX
PD 12-OCT-2001.
XX
PF 11-APR-2000; 2000FR-00004630.
XX
PR 11-APR-2000; 2000FR-00004630.
XX
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX
PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;
XX
XX WPI; 2002-043418/06.
XX
XX New nucleotide sequence useful in the identification of Lactococcus
XX lactis and related species.
XX
XX Claim 6; SEQ ID NO 286; 2504pp; French.
XX
CC The present invention is related to a Lactococcus lactis nucleotide
CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic
CC acid sequence is useful in the detection and/or amplification of nucleic
CC acid sequence, particularly to identify Lactococcus lactis or related
CC species. The proteins of the invention are useful for the biosynthesis or
CC biodegradation of a composition of interest. The invention helps research
CC in lactic bacteria, particularly useful in the production of yogurt and
CC cheese. Note: The sequence data for this patent is based on equivalent
CC patent WO20017734 (published 18-OCT-2001) which is available in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 288 AA;

Query Match 8.2%; Score 23; DB 5; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 SPFELSGGQMRRAIAGILAMEP 164
DB 141 SPFELSGGQMRRAIAGILAMEP 163

RESULT 9
ADK99877
ID ADK99877 standard; protein; 279 AA.
XX
XX AC ADK99877;
XX
DT 20-MAY-2004 (first entry)
XX
DE Streptococcus agalactiae ORF SAG2150-related protein 3.
XX
XX immunogenic composition; group B Streptococcus; GBS; antibacterial;
XX streptococcal infection; vaccine; SAG.
XX
XX Streptococcus agalactiae.
XX
XX WO2004018646-A2.
XX
XX 04-MAR-2004.
XX
XX 26-AUG-2003; 2003WO-US026827.
XX
XX 26-AUG-2002; 2002US-0406237P.
XX 27-AUG-2002; 2002US-0406676P.
XX 28-AUG-2002; 2002US-0406757P.
XX


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PA (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX Tettelin H, Maignani V;
XX WPI; 2004-248071/23.
XX Immunogenic composition useful as a vaccine for treating or preventing
PT streptococcal infections, comprises group B Streptococcus polypeptides.
XX Claim 10; SEQ ID NO 7914; 1194pp; English.
XX The invention relates to a novel immunogenic composition comprising a
XX combination of 2-5 group B Streptococcus (GBS) polypeptides. Each
XX polypeptide is encoded by a GBS polynucleotide sequence which is
XX homologous to a polynucleotide sequence of group A Streptococcus (GAS),
XX Streptococcus pneumoniae and/or at least one other GBS serotype. The
XX composition of the invention demonstrates antibacterial activity whilst
XX the polypeptides and polynucleotides may be useful in assays to diagnose
XX and identify streptococcal infections or for identifying, screening and
XX developing vaccines and other treatments for streptococcal infections.
XX The current sequence is that of a Streptococcus agalactiae ORF SAG
XX protein of the invention.
XX Sequence 279 AA;
SQ

```

Query Match 7.9%; Score 22; DB 8; Length 279;
 Best Local Similarity 100.0%; Pred. No. 1.4e-12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 143 PFELSGGQMRRAIAGILAMEP 164
Db 142 PFELSGGQMRRAIAGILAMEP 163

```

RESULT 11
 ADK99876
 ID ADK99876 standard; protein; 279 AA.
 AC ADK99876;
 XX 20-MAY-2004 (first entry)
 DT Streptococcus agalactiae ORF SAG2150-related protein 2.
 DE immunogenic composition; group B Streptococcus; GBS; antibacterial;
 KW streptococcal infection; vaccine; SAG.
 XX Streptococcus agalactiae.
 OS WO2004018646-A2.
 FN 04-MAR-2004.
 PD 26-AUG-2003; 2003WO-US026827.
 XX 26-AUG-2002; 2002US-0406237P.
 PR 27-AUG-2002; 2002US-0406676P.
 FR 28-AUG-2002; 2002US-0406757P.
 XX (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX Tettelin H, Maignani V;
 PI WPI; 2004-248071/23.
 DR Immunogenic composition useful as a vaccine for treating or preventing
 XX streptococcal infections, comprises group B Streptococcus polypeptides.
 XX Claim 10; SEQ ID NO 7913; 1194pp; English.
 XX The invention relates to a novel immunogenic composition comprising a
 XX combination of 2-5 group B Streptococcus (GBS) polypeptides. Each
 XX polypeptide is encoded by a GBS polynucleotide sequence which is
 XX homologous to a polynucleotide sequence of group A Streptococcus (GAS),
 XX Streptococcus pneumoniae and/or at least one other GBS serotype. The
 XX composition of the invention demonstrates antibacterial activity whilst
 XX the polypeptides and polynucleotides may be useful in assays to diagnose
 XX and identify streptococcal infections or for identifying, screening and
 XX developing vaccines and other treatments for streptococcal infections.
 XX The current sequence is that of a Streptococcus agalactiae ORF SAG
 XX protein of the invention.
 XX Sequence 279 AA;
 SQ

Query Match 7.9%; Score 22; DB 8; Length 279;
 Best Local Similarity 100.0%; Pred. No. 1.4e-12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 143 PFELSGGQMRRAIAGILAMEP 164
Db 142 PFELSGGQMRRAIAGILAMEP 163

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RESULT 10
 ADK99878
 ID ADK99878 standard; protein; 279 AA.
 AC ADK99878;
 XX 20-MAY-2004 (first entry)
 DT Streptococcus agalactiae ORF SAG2150-related protein 4.
 DE immunogenic composition; group B Streptococcus; GBS; antibacterial;
 KW streptococcal infection; vaccine; SAG.
 XX Streptococcus agalactiae.
 OS WO2004018646-A2.
 FN 04-MAR-2004.
 PD 26-AUG-2003; 2003WO-US026827.
 XX 26-AUG-2002; 2002US-0406237P.
 PR 27-AUG-2002; 2002US-0406676P.
 FR 28-AUG-2002; 2002US-0406757P.
 XX (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX Tettelin H, Maignani V;
 PI WPI; 2004-248071/23.
 DR Immunogenic composition useful as a vaccine for treating or preventing
 XX streptococcal infections, comprises group B Streptococcus polypeptides.
 XX Claim 10; SEQ ID NO 7915; 1194pp; English.
 XX The invention relates to a novel immunogenic composition comprising a

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Query Match      7.9%; Score 22; DB 8; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 PFELSGGQMRVAIAGILAMEP 164
Db 142 PFELSGGQMRVAIAGILAMEP 163

RESULT 12
ADK99880
ID ADK99880 standard; protein; 279 AA.
AC ADK99880;
XX
XX
XX 20-MAY-2004 (first entry)
XX
XX Streptococcus agalactiae ORF SAG2150-related protein 6.
DE
XX immunogenic composition; group B Streptococcus; GBS; antibacterial;
KW streptococcal infection; vaccine; SAG.
XX
XX Streptococcus agalactiae.
OS
XX WO2004018646-A2.
PN
XX
XX 04-MAR-2004.
PD
XX
XX 26-AUG-2003; 2003WO-US026827.
PF
XX
XX 26-AUG-2002; 2002US-0406237P.
PR
XX 27-AUG-2002; 2002US-0406676P.
PR
XX 28-AUG-2002; 2002US-0406757P.
PR
XX
XX (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
XX Tettelin H, Massignani V;
PI
XX WPI; 2004-248071/23.
XX
XX Immunogenic composition useful as a vaccine for treating or preventing
PT streptococcal infections, comprises group B Streptococcus polypeptides.
XX
XX Claim 10; SEQ ID NO 7917; 1194pp; English.
XX
XX The invention relates to a novel immunogenic composition comprising a
CC combination of 2-5 group B Streptococcus (GBS) polypeptides. Each
CC polypeptide is encoded by a GBS polynucleotide sequence which is
CC homologous to a polynucleotide sequence of group A Streptococcus (GAS),
CC Streptococcus pneumoniae and/or at least one other GBS serotype. The
CC composition of the invention demonstrates antibacterial activity whilst
CC the polypeptides and polynucleotides may be useful in assays to diagnose
CC and identify streptococcal infections or for identifying, screening and
CC developing vaccines and other treatments for streptococcal infections.
CC The current sequence is that of a Streptococcus agalactiae ORF SAG
CC protein of the invention.
XX
XX SQ Sequence 279 AA;
XX
XX Query Match      7.9%; Score 22; DB 8; Length 279;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-12;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 PFELSGGQMRVAIAGILAMEP 164
Db 142 PFELSGGQMRVAIAGILAMEP 163

RESULT 14
ADK99883
ID ADK99883 standard; protein; 279 AA.
XX
XX ADK99883;
XX
XX 20-MAY-2004 (first entry)
XX
XX Streptococcus agalactiae ORF SAG2150-related protein 9.
DE
XX immunogenic composition; group B Streptococcus; GBS; antibacterial;
KW streptococcal infection; vaccine; SAG.
XX
XX Streptococcus agalactiae.
OS
XX WO2004018646-A2.
PN
XX
XX

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Db 1 MGIALENVNFYQEGTPLASALSVDLSLTIEDGYSYALIGHTGSGKSTILQLLGLLVP 60
Qy 61 QGSVRVFTLTITSTSKNDIRQIRKQVGLVQFAENQIFETVLKDVAFGPNFGVSEED 120
Db 61 QGSVRVFTLTITSTSKNDIRQIRKQVGLVQFAENQIFETVLKDVAFGPNFGVSEED 120
Qy 121 AVKTAREKALVIGIDESLFDSPPELGGQWRRVAIAGILAMEPAILVLDSPTAGLDP 180
Db 121 AVKTAREKALVIGIDESLFDSPPELGGQWRRVAIAGILAMEPAILVLDSPTAGLDP 180
Qy 181 RKEMLTLFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRVKGKPSDVFDQVPM 240
Db 181 RKEMLTLFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRVKGKPSDVFDQVPM 240
Qy 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279
Db 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279

RESULT 2
QSDMYO PRELIMINARY; PRT; 279 AA.
AC QSDMYO;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Hypothetical protein ABC-NBP.
GN Name=ABC-NBP; OrderedLocusNames=spr2025;
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OC NCBI_TaxID=171101;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21429245; PubMed=11544234;
RX DOI=10.1128/JB.183.19.5709-5717.2001;
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
RA Dehoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmore R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McAhren S.M., McHenry M., Mcleaster K., Mundy C.W., Nicas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostek P.R. Jr., Skatrud P.L.,
RA Glass J.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
RL J. Bacteriol. 183:5709-5717(2001).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE008566; AAL00827.1; -.
DR PIR; F98124; F98124.
DR HSP; P02915; I800.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC tran; 1.
DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 279 AA; 30553 MW; FB5A148C367A6032 CRC64;

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Query Match 99.4%; Score 1378; DB 2; Length 279;
Best Local Similarity 99.3%; Pred. No. 2.7e-87;
Matches 277; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGIALENVNFYQEGTPLASALSVDLSLTIEDGYSYALIGHTGSGKSTILQLLGLLVP 60
Db 1 MGIALENVNFYQEGTPLASALSVDLSLTIEDGYSYALIGHTGSGKSTILQLLGLLVP 60

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Qy 61 QGSVRVFTLTITSTSKNDIRQIRKQVGLVQFAENQIFETVLKDVAFGPNFGVSEED 120
Db 61 QGSVRVFTLTITSTSKNDIRQIRKQVGLVQFAENQIFETVLKDVAFGPNFGVSEED 120
Qy 121 AVKTAREKALVIGIDESLFDSPPELGGQWRRVAIAGILAMEPAILVLDSPTAGLDP 180
Db 121 AVKTAREKALVIGIDESLFDSPPELGGQWRRVAIAGILAMEPAILVLDSPTAGLDP 180
Qy 181 RKEMLTLFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRVKGKPSDVFDQVPM 240
Db 181 RKEMLTLFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRVKGKPSDVFDQVPM 240
Qy 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279
Db 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279

RESULT 3
QSDRSO PRELIMINARY; PRT; 280 AA.
AC QSDRSO;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Putative ABC transporter, ATP-binding protein; possible cobalt
DE transport system.
GN OrderedLocusNames=SMU.2149c;
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OC NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=UAI59 / ATCC 700610 / Serotype c;
RX MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
RX Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RX Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
RX Qian Y., Li S., Zhu H., Najjar F.Z., Lai H., White J., Roe B.A.,
RX Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UAI59, a cariogenic dental
RT pathogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE015035; AAN59738.1; -.
DR HSP; P58301; I058.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC tran; 1.
DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 280 AA; 30941 MW; 600ED3F5CC6F928A CRC64;

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Query Match 72.3%; Score 1002.5; DB 2; Length 280;
Best Local Similarity 70.0%; Pred. No. 2.3e-61;
Matches 196; Conservative 38; Mismatches 45; Indels 1; Gaps 1;

Qy 1 MGIALENVNFYQEGTPLASALSVDLSLTIEDGYSYALIGHTGSGKSTILQLLGLLVP 60
Db 1 MGIALENVNFYQEGTPLASALSVDLSLTIEDGYSYALIGHTGSGKSTILQLLGLLVP 60
Qy 61 QGSVRVFTLTITSTSKNDIRQIRKQVGLVQFAENQIFETVLKDVAFGPNFGVSEED 120
Db 61 EGTVLVDVAIRSDSKNDIKIRKQVGLVQFPFESQLFDETVLKDVAFGPNFGISKEE 120

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QY 121 AVKTAREKALVGDIDSLFDRSPFELSGGQRRVAIAGILAMEPAILVLDEPTAGLDPLG 180
 DB 121 AEKJAREKALVGISEELFEKPFELSGGQRRVAIAGILAMEPAILVLDEPTAGLDPLG 180
 QY 181 RKELMTLTKKHLQSGMTIVLVTHLMDVVAQYVYVMEKGRVKGKPSDFQDVVFME 240
 DB 181 RRELMTLTKKHLQSGMTIVLVTHLMDVVAQYVYVMEKGRVKGKPSDFQDVVFME 240
 QY 241 EVOLGVPKITAFCKRLADRGVSFKLPIKIEPKESL-NG 279
 DB 241 SKQLGVPKITQFAAHLRERGITFDALPITLBEFVEAIRNG 280

RESULT 4

Q99X12 ID Q99X12 PRELIMINARY; PRT; 280 AA.
 AC Q99X12;
 DT 01-JUN-2001 (TREMELrel. 17, Created)
 DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Putative ABC transporter (ATP-binding protein).
 GN OrderedLocusNames=SPY21194;
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
 RX MEDLINE=21192694; PubMed=1196296; DOI=10.1073/pnas.071559398;
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
 RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; A006636; AAK34822.1; -;
 DR HSSP; Q58663; IGX.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR Pfam; PF00005; ABC_tran; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
 KW ATP-binding; Complete proteome.
 SQ SEQUENCE 280 AA; 30863 MW; DBE44F6F8780C7D5 CRC64;

Query Match 70.08; Score 971; DB 2; Length 280;
 Best Local Similarity 69.08; Pred. No. 3.5e-59;
 Matches 191; Conservative 35; Mismatches 51; Indels 0; Gaps 0;
 QY 1 MGIALENVNFTYQEGTGPLASALSDVLTIEDGSYTALIGHTGSGKSTILQLLGLVPS 60
 DB 1 MSINLQNVSYTYQAGTFPEGRALFNINLDLDSYTAFTIGHTGSGKSTIMQLLGLHVPT 60
 QY 61 QGSRVRFDTLITSTSKNDIRQIRKQVGLVFPQFAENQIFETVLKDVAFQPNFGVSEED 120
 DB 61 TGIVSVNDKQDITNHSKNKEIKSRKHVGLVFPQFESQLEETVLKDVAFQPNFGVSP 120
 QY 121 AVKTAREKALVGDIDSLFDRSPFELSGGQRRVAIAGILAMEPAILVLDEPTAGLDPLG 180
 DB 121 AEALAREKALVGISENLPEKNPFELSGGQRRVAIAGILAMQPKVLVLDEPTAGLDPLG 180
 QY 181 RKELMTLTKKHLQSGMTIVLVTHLMDVVAQYVYVMEKGRVKGKPSDFQDVVFME 240
 DB 181 RRELMTLTKKHLQSGMTIVLVTHLMDVVAQYVYVMEKGRVKGKPSDFQDVVFME 240

QY 241 EVOLGVPKITAFCKRLADRGVSFKLPIKIEPKESL 277
 DB 241 KKQLGVPKVTKLAQRLVDRGIPISLPTLLEBELREV 277

RESULT 5

Q7CMW8 ID Q7CMW8 PRELIMINARY; PRT; 280 AA.
 AC Q7CMW8;
 DT 05-JUL-2004 (TREMELrel. 27, Created)
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
 DE Putative ABC transporter (ATP-binding protein).
 GN OrderedLocusNames=spym18 2229;
 OS Streptococcus pyogenes (serotype M18).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=186103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MGAS8232;
 RX MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;
 RA Smoot J.C., Barbican K.D., Van Compel J.J., Smoot L.M., Chaussee M.S.,
 RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
 RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
 RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
 RT "Genome sequence and comparative microarray analysis of serotype M18
 group A Streptococcus strains associated with acute rheumatic fever
 outbreaks.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; A010123; AAL98661.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR Pfam; PF00005; ABC_tran; 1.
 DR PROSITE; PS00006; ABC_TRANSPORTER; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
 KW ATP-binding; Complete proteome.
 SQ SEQUENCE 280 AA; 30863 MW; DBE44F6F8780C7D5 CRC64;

Query Match 70.08; Score 971; DB 2; Length 280;
 Best Local Similarity 69.08; Pred. No. 3.5e-59;
 Matches 191; Conservative 35; Mismatches 51; Indels 0; Gaps 0;
 QY 1 MGIALENVNFTYQEGTGPLASALSDVLTIEDGSYTALIGHTGSGKSTILQLLGLVPS 60
 DB 1 MSINLQNVSYTYQAGTFPEGRALFNINLDLDSYTAFTIGHTGSGKSTIMQLLGLHVPT 60
 QY 61 QGSRVRFDTLITSTSKNDIRQIRKQVGLVFPQFAENQIFETVLKDVAFQPNFGVSEED 120
 DB 61 TGIVSVNDKQDITNHSKNKEIKSRKHVGLVFPQFESQLEETVLKDVAFQPNFGVSP 120
 QY 121 AVKTAREKALVGDIDSLFDRSPFELSGGQRRVAIAGILAMEPAILVLDEPTAGLDPLG 180
 DB 121 AEALAREKALVGISENLPEKNPFELSGGQRRVAIAGILAMQPKVLVLDEPTAGLDPLG 180
 QY 181 RKELMTLTKKHLQSGMTIVLVTHLMDVVAQYVYVMEKGRVKGKPSDFQDVVFME 240
 DB 181 RRELMTLTKKHLQSGMTIVLVTHLMDVVAQYVYVMEKGRVKGKPSDFQDVVFME 240
 QY 241 EVOLGVPKITAFCKRLADRGVSFKLPIKIEPKESL 277
 DB 241 KKQLGVPKVTKLAQRLVDRGIPISLPTLLEBELREV 277

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RESULT 6
Q8K5H2 PRELIMINARY; PRT; 280 AA.
ID Q8K5H2; Q79VY7;
AC 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Putative ABC transporter (ATP-binding protein).
GN OrderedLocNames=SPa1841, SpvM3.1845;
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OX NCBI_TaxID=198466;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RA MEDLINE=22133808; PubMed=1212206; DOI=10.1073/pnas.152298499;
RX Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=SSI-1;
RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Taniyasu Y.,
RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
RA Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights
RT into phage evolution.";
RL Genome Res. 13:1042-1055(2003).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AF014172; AAM80452.1; -.
DR EMBL; AF005146; BAC64936.1; -.
DR HSP; Q58663; 1G9X.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC tran_1.
DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 280 AA; 30905 MW; 8E7752BD48834752 CRC64;

Query Match 69.9%; Score 969; DB 2; Length 280;
Best Local Similarity 68.6%; Pred. No. 4.7e-59;
Matches 190; Conservative 36; Mismatches 51; Indels 0; Gaps 0;

QY 1 MGIALENNFTYQGTPLASALSDVSLTIEDGSYTALIGHTGSGKSTILQLLGLVPS 60
Db 1 MGINLQNSYTYQVGTPEGRALFNILNDLDSYTAFTIGHTGSGKSTIMQLLGLHPT 60

QY 61 QGSVRVFDTLTTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFGPNFGVSEED 120
Db 61 TGIVSVQKQDITNHSKNKEIKIRKHVGLVFOFPESQLFEETVLKDVAFGPNFGISPEE 120

QY 121 AVKTAREKALVIGIDESLFDPSFPELSCGQMRRAIAGILAMEPAILVLDDEPTAGLDPLG 180
Db 121 TGIVSVQKQDITNHSKNKEIKIRKHVGLVFOFPESQLFEETVLKDVAFGPNFGISPEE 120

QY 181 RKLMTLFPKLLHQSGMTIVLTHLMDVAVYANQVYVMEKRLVKGKPSDFVQDVWFE 240
Db 181 ABALAREKALVIGISENLFKPNPFELSCGQMRRAIAGILAMEPAILVLDDEPTAGLDPLG 180

QY 181 RKLMTLFPKLLHQSGMTIVLTHLMDVAVYANQVYVMEKRLVKGKPSDFVQDVWFE 240
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Db 181 RKLMTLFPKLLHQSGMTIVLTHLMDVAVYANQVYVMEKRLVKGKPSDFVQDVWFE 240
QY 241 EVQLGVPKITAFCRLADRGVSPKRLPIKIEEPKESL 277
Db 241 KQQLGVPKVTKLAQLVDRGIPISLSLITLLEBELREV 277

RESULT 7
Q8DMR4 PRELIMINARY; PRT; 280 AA.
ID Q8DMR4;
AC Q8DMR4;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE ABC transporter, ATP-binding protein.
GN OrderedLocNames=SAG2150;
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OX NCBI_TaxID=216466;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=2222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
RA Tetelin H., Masignani V., Cielesiewicz M.J., Eisen J.A., Peterson S.N.,
RA Wessels M.R., Paulsen I.T., Neilson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radu D., Fedorova N.B., Scanlan D., Khouir H.M., Mulligan S.,
RA Cardy H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE014289; AAN01008.1; -.
DR HSP; P58301; 1US8.
DR TIGR; SAG2150; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC tran; 1.
DR ProDom; PD000006; ABC transporter; 1.
DR PROSITE; PS00211; ABC TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 280 AA; 31111 MW; 00253EF4A7E5C30B CRC64;

Query Match 68.3%; Score 948; DB 2; Length 280;
Best Local Similarity 66.8%; Pred. No. 1.3e-57;
Matches 185; Conservative 39; Mismatches 53; Indels 0; Gaps 0;

QY 1 MGIALENNFTYQGTPLASALSDVSLTIEDGSYTALIGHTGSGKSTILQLLGLVPS 60
Db 1 MGISFKNYSYTYQAGTPEGRALFDVNLKIEDASYTAFTIGHTGSGKSTIMQLLGLHPT 60

QY 61 QGSVRVFDTLTTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFGPNFGVSEED 120
Db 61 KGRVIVDDFSIKAGKNKEIKIRKHVGLVFOFPESQLFEETVLKDVAFGPNFGISQIE 120

QY 121 AVKTAREKALVIGIDESLFDPSFPELSCGQMRRAIAGILAMEPAILVLDDEPTAGLDPLG 180
Db 121 AERLAEEKLVLGISEDLFDKNPFELSCGQMRRAIAGILAMEPAILVLDDEPTAGLDPLG 180

QY 181 RKLMTLFPKLLHQSGMTIVLTHLMDVAVYANQVYVMEKRLVKGKPSDFVQDVWFE 240
Db 181 RKLMTLFPKLLHQSGMTIVLTHLMDVAVYANQVYVMEKRLVKGKPSDFVQDVWFE 240

QY 241 EVQLGVPKITAFCRLADRGVSPKRLPIKIEEPKESL 277
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[illegible]

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OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis."
RL Science 299:2071-2074 (2003).
CC -I- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE016947; AA080106.1; -.
DR HSP; Q58206; IL2T.
DR TIGR; EF0238; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR Pfam; PF00005; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Complete proteome.
KW SEQUENCE 291 AA; 32575 MW; F1B0DC04824B2F05 CRC64;
SQ
Query Match 61.3%; Score 850.5; DB 2; Length 291;
Best Local Similarity 57.9%; Pred. No. 7.5e-51;
Matches 161; Conservative 54; Mismatches 62; Indels 1; Gaps 1;
QY 1 MGIALENVFTYQEGTPLASALSVSITIEDGYSYALTIQSGKSTILQNLGLVPS 60
DB 3 MDIRKQVDFTYQNTPEQRALFINLTIQGSIYTAIVGHTSGKSTLLQHNALVKPT 62
QY 61 QGSVRFDTLTSTSKNDIRKQVGLVFOFPAENQIFETVLKDVAFGPNQFVSEED 120
DB 63 KQQVITIGRVITPDTNKNLKPIRKQVGLVFOFPAENQIFETVLKDVAFGPNQFVSEED 122
QY 121 AVKTAREKALVGDSELPDRSPFELSGQMRVAIAGILAMEPAIILVLDPTAGLDPLG 180
DB 123 AKKLAKMLDLVGLDEKYLQHSFPFELSGQMRVAIAGILAMEPEVLVLDPTAGLDPLG 182
QY 181 RKELMTLFFKLLH-QSGMTIVLVTHLMDVVAEYANQVYMEKGRVKGKPSDVQDVVFM 239
DB 183 RKEMMEMSRLKHEHMTIVLVTHLMDVVAEYANQVYMEKGRVKGKPSDVQDVVFM 242
QY 240 EVQGVGPKITAFCKRLADRGVSFKRLPIKIEEFKESL 277
DB 243 KEKQLGVPTAAEFAEKLVAKGFSEQLPLTADQLADQL 280
RESULT 11
Q88XV1
ID Q88XV1 PRELIMINARY; PRT; 295 AA.
AC Q88XV1;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE ABC transporter, ATP-binding protein.
GN OrderedLocusNames=lp_1074;
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis."
RL Science 299:2071-2074 (2003).
CC -I- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE016947; AA080106.1; -.
DR HSP; Q58206; IL2T.
DR TIGR; EF0238; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR Pfam; PF00005; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Complete proteome.
KW SEQUENCE 291 AA; 32575 MW; F1B0DC04824B2F05 CRC64;
SQ
Query Match 61.3%; Score 850.5; DB 2; Length 291;
Best Local Similarity 57.9%; Pred. No. 7.5e-51;
Matches 161; Conservative 54; Mismatches 62; Indels 1; Gaps 1;
QY 1 MGIALENVFTYQEGTPLASALSVSITIEDGYSYALTIQSGKSTILQNLGLVPS 60
DB 3 MDIRKQVDFTYQNTPEQRALFINLTIQGSIYTAIVGHTSGKSTLLQHNALVKPT 62
QY 61 QGSVRFDTLTSTSKNDIRKQVGLVFOFPAENQIFETVLKDVAFGPNQFVSEED 120
DB 63 KQQVITIGRVITPDTNKNLKPIRKQVGLVFOFPAENQIFETVLKDVAFGPNQFVSEED 122
QY 121 AVKTAREKALVGDSELPDRSPFELSGQMRVAIAGILAMEPAIILVLDPTAGLDPLG 180
DB 123 AKKLAKMLDLVGLDEKYLQHSFPFELSGQMRVAIAGILAMEPEVLVLDPTAGLDPLG 182
QY 181 RKELMTLFFKLLH-QSGMTIVLVTHLMDVVAEYANQVYMEKGRVKGKPSDVQDVVFM 239
DB 183 RKEMMEMSRLKHEHMTIVLVTHLMDVVAEYANQVYMEKGRVKGKPSDVQDVVFM 242
QY 240 EVQGVGPKITAFCKRLADRGVSFKRLPIKIEEFKESL 277
DB 243 KEKQLGVPTAAEFAEKLVAKGFSEQLPLTADQLADQL 280
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P70970
ID P70970 PRELIMINARY; PRT; 276 AA.
AC P70970; Q79752;
DT 01-PEB-1997 (TRENBLrel. 02, Created)
DT 01-PEB-1997 (TRENBLrel. 02, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein orf5 (yba5 protein).
GN Name=orf5; Synonyms=yba5; OrderedLocusNames=BSU01460;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97124188; PubMed=8969501;
RA Yasumoto K., Liu H., Jeong S.M., Ohashi Y., Kakinuma S., Tanaka K.,
RA Kawamura F., Yoshikawa H., Takahashi H.;
RT "Sequence analysis of a 50 kb region between spoOH and rrrH on the
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OM protein - protein search, using sw model

Run on: October 28, 2005, 18:07:29 ; Search time 40 Seconds
(without alignments)

671.112 Million cell updates/sec

Title: US-09-769-744D-26

Perfect score: 279

Sequence: 1 MGIALENVNTYQEGTPLAS.....GVSPKRLPIKIEPKESLNG 279

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	279	100.0	279	2	C95459
2	167	59.9	279	2	F98124
3	23	8.2	288	2	F86659
4	19	6.8	276	2	E69742
5	18	6.5	288	2	AH1399
6	18	6.5	288	2	AG1775
7	13	4.7	183	2	T44413
8	13	4.7	282	2	E83670
9	12	4.3	304	2	C92598
10	11	3.9	253	2	G72560
11	11	3.9	279	2	G64435
12	11	3.9	300	2	S34187
13	10	3.6	178	2	S77760
14	10	3.6	264	2	G83245
15	10	3.6	268	2	AG1325
16	10	3.6	268	2	AI1578
17	10	3.6	271	2	AG0757
18	10	3.6	277	2	T45265
19	10	3.6	278	2	F87536
20	10	3.6	284	2	T35723
21	10	3.6	286	2	F97281
22	10	3.6	286	2	G82698
23	10	3.6	303	2	G62814
24	10	3.6	304	2	I64219
25	10	3.6	307	2	T36000
26	10	3.6	311	2	A69095
27	10	3.6	433	2	D82879
28	10	3.6	601	2	F83790
29	9	3.2	210	2	S76316

30	9	3.2	224	2	AE1999
31	9	3.2	242	2	F84315
32	9	3.2	260	2	S75010
33	9	3.2	260	2	S74597
34	9	3.2	260	2	AD1829
35	9	3.2	278	2	T44412
36	9	3.2	280	2	T03543
37	9	3.2	285	2	F69375
38	9	3.2	286	2	H90018
39	9	3.2	288	2	D83731
40	9	3.2	293	2	AI2139
41	9	3.2	294	2	D87691
42	9	3.2	364	2	T02364
43	9	3.2	472	2	D98199
44	9	3.2	496	2	AE0305
45	9	3.2	500	2	AE3087
46	9	3.2	508	2	G95421
47	9	3.2	554	2	E70435
48	9	3.2	565	2	E86665
49	9	3.2	590	2	A84986
50	9	3.2	593	2	AI0559
51	9	3.2	593	2	A64775
52	9	3.2	593	2	G90691
53	9	3.2	605	2	S85542
54	9	3.2	607	2	AH0381
55	9	3.2	611	2	E86657
56	9	3.2	697	2	G70704
57	9	3.2	724	2	B87015
58	9	3.2	726	2	T44905
59	9	3.2	726	2	E70203
60	9	3.2	950	2	E70203
61	9	3.2	1143	4	I84547
62	9	3.2	2410	1	JQ1948
63	9	3.2	2412	1	JQ1537
64	8	2.9	215	2	I56135
65	8	2.9	216	2	E81247
66	8	2.9	222	2	AG3483
67	8	2.9	231	2	A96031
68	8	2.9	231	2	AH2872
69	8	2.9	231	2	B97649
70	8	2.9	237	2	A69255
71	8	2.9	238	2	G96929
72	8	2.9	248	2	AG2969
73	8	2.9	248	2	G69352
74	8	2.9	250	2	AG2885
75	8	2.9	250	2	D97661
76	8	2.9	252	2	F97072
77	8	2.9	259	2	F86843
78	8	2.9	259	2	H97301
79	8	2.9	274	2	AH1319
80	8	2.9	274	2	AH1691
81	8	2.9	275	2	D98313
82	8	2.9	311	2	F87655
83	8	2.9	382	2	AG3533
84	8	2.9	385	2	F95161
85	8	2.9	385	2	E98027
86	8	2.9	390	2	AE2576
87	8	2.9	420	2	C72720
88	8	2.9	428	2	C86770
89	8	2.9	506	2	A82876
90	8	2.9	507	2	D98330
91	8	2.9	507	2	AI2952
92	8	2.9	510	2	AI0490
93	8	2.9	540	2	A82083
94	8	2.9	543	2	E89839
95	8	2.9	557	2	C84146
96	8	2.9	571	2	S58356
97	8	2.9	583	2	T39112
98	8	2.9	583	2	G95214
99	8	2.9	583	2	F98078
100	8	2.9	595	2	T31077
101	8	2.9	601	2	AC1281
102	8	2.9	601	2	AB1644

ATP-binding protei
cobalt transport A
ABC-type transport
ABC-type transport
ATP-binding protei
ABC transporter (A
ABC transporter (A
probable cobalt tr
hypothetical prote
ABC transporter, A
ABC transporter (A
ABC transporter syst
ABC transporter, A
hypothetical prote
hypothetical prote
probable sugar tra
hypothetical prote
probable ABC trans
ABC transporter (M
ABC transporter AT
mdLB [imported] -
probable ABC trans
ABC-type transport
ABC-type transport
ABC-type transport
probable ATP trans
ABC transporter AT
hypothetical prote
ABC transporter ML
ABC-type transport
exonuclease SbcC (
hypothetical mdl f
genome polyprotein
interleukin 12 p35
cell division AP3
heme exporter prot
probable ureashort
hypothetical prote
probable ATP-bind
polysaccharide ABC
ABC transporter AT
hypothetical prote
branched-chain ami
hypothetical prote
oligopeptide trans
ABC transporter, A
ABC transporter, A
ABC-type MDR trans
ferrichrome ABC tr
ferrichrome ABC tr
glutamine ABC tran
ABC transporter, A
spermidine/putresc
hypothetical prote
hypothetical prote
hypothetical prote
probable oligopept
hypothetical prote
oligopeptide trans
hypothetical prote
hypothetical prote
sugar transport AT
conserved hypothet
hypothetical prote
ABC transporter re
pept protein - Sta
probable amidase -
ABC transporter, A
hypothetical prote
probable ABC-trans
ABC transporter (A
ABC transporter (A

103	8	2.9	606	2	JM0054	amiloride-sensitiv	176	7	2.5	276	2	T36288	probable ABC-type
104	8	2.9	606	2	AC2425	ATP-binding protei	177	7	2.5	277	2	E71545	probable oligopept
105	8	2.9	608	2	H86783	hypothetical prote	178	7	2.5	278	2	E65020	ethanolamine utili
106	8	2.9	636	2	C81128	ABC transporter, A	179	7	2.5	278	2	D91043	ethanolamine utili
107	8	2.9	646	1	E71536	probable transporter	180	7	2.5	278	2	G85887	ethanolamine utili
108	8	2.9	650	2	A11333	ABC transporter (A	181	7	2.5	279	2	AC0814	probable ethanolam
109	8	2.9	650	2	AH1704	ABC transporter (A	182	7	2.5	279	2	E97068	cobalt transport (
110	8	2.9	673	2	H69828	ABC transporter (A	183	7	2.5	279	2	A11399	ABC transporter (A
111	8	2.9	674	2	F83794	ABC transporter (A	184	7	2.5	279	2	AH1775	phosphate abc tran
112	8	2.9	677	2	T10657	probable ABC-type	185	7	2.5	280	2	E75082	cobalt transporter A
113	8	2.9	680	2	T10656	probable ABC-type	186	7	2.5	280	2	G69043	abc transporter, A
114	8	2.9	690	2	S54211	ATM1 protein precu	187	7	2.5	280	2	H75151	ABC transporter, A
115	8	2.9	820	2	B83739	exinuclease ABC (188	7	2.5	283	2	E82662	ABC transporter AT
116	8	2.9	1323	2	T18214	ATP binding casset	189	7	2.5	284	2	F81563	peptide ABC transp
117	7	2.5	89	1	S38882	ribosomal protein	190	7	2.5	284	2	G72107	oligopeptide trans
118	7	2.5	95	2	H69341	conserved hypothet	191	7	2.5	284	2	A86516	oligopeptide trans
119	7	2.5	104	2	T36976	probable transposa	192	7	2.5	284	2	G28139	sulfate transport
120	7	2.5	134	2	T36750	probable gntR-fami	193	7	2.5	284	2	E62839	ABC transport prot
121	7	2.5	143	2	B69782	hypothetical prote	194	7	2.5	284	2	G71192	probable cobalt tr
122	7	2.5	150	2	B98044	ABC transporter, t	195	7	2.5	285	2	E87517	pantoate-beta-alan
123	7	2.5	153	2	C46036	ERK2 homolog - fru	196	7	2.5	292	2	H69999	ABC transporter (A
124	7	2.5	162	2	T16163	hypothetical prote	197	7	2.5	294	2	E82879	ABC transporter UU
125	7	2.5	174	2	G95096	DNA topology modul	198	7	2.5	305	2	F82303	ABC transporter, A
126	7	2.5	176	2	A2484	hypothetical prote	199	7	2.5	306	2	T36764	probable ABC-type
127	7	2.5	176	2	G70658	probable aroK prot	200	7	2.5	307	2	F87952	protein T2683.4 [i
128	7	2.5	181	2	B70704	probable rocd - My	201	7	2.5	307	2	C83188	probable ATP-bindi
129	7	2.5	183	2	A12926	conserved hypothet	202	7	2.5	308	2	D80524	hypothetical ABC t
130	7	2.5	183	2	F98355	hypothetical prote	203	7	2.5	308	2	D97589	probable ATP-bindi
131	7	2.5	197	2	C69877	adenylsulfate ki	204	7	2.5	308	2	A12810	hypothetical prote
132	7	2.5	200	2	AD3220	conserved hypothet	205	7	2.5	308	2	H64980	hypothetical ABC t
133	7	2.5	201	2	F97035	p-loop kinase (uri	206	7	2.5	308	2	S45204	probable ABC-type
134	7	2.5	206	2	H84978	adenylsulfate k	207	7	2.5	308	2	C85496	hypothetical prote
135	7	2.5	206	2	AF2299	cobalt transport A	208	7	2.5	308	2	C90645	hypothetical prote
136	7	2.5	208	2	A84073	adenylsulfate ki	209	7	2.5	308	2	H81005	hypothetical prote
137	7	2.5	209	2	E64172	hypothetical prote	210	7	2.5	308	2	A95850	hypothetical prote
138	7	2.5	230	2	D69858	ABC transporter (A	211	7	2.5	308	2	AH0413	probable ABC trans
139	7	2.5	231	2	AG3225	hypothetical prote	212	7	2.5	309	2	T35756	probable branched
140	7	2.5	232	2	AE2049	ATP-binding protei	213	7	2.5	310	2	G82707	ABC transporter AT
141	7	2.5	233	2	B81076	thermonuclease fam	214	7	2.5	310	2	B83294	probable ATP-bindi
142	7	2.5	237	2	A72688	probable high-affi	215	7	2.5	311	2	B95202	methionyl-tRNA for
143	7	2.5	238	2	B84967	hypothetical prote	216	7	2.5	311	2	B98069	methionyl-tRNA for
144	7	2.5	240	2	A11532	two-component resp	217	7	2.5	311	2	AC1158	ABC transporter (A
145	7	2.5	240	2	T25299	hypothetical prote	218	7	2.5	311	2	AH1516	ABC transporter (A
146	7	2.5	240	2	D74415	zinc ABC transport	219	7	2.5	312	2	G97382	probable ATP-bindi
147	7	2.5	246	2	A69666	Na+ ABC transporte	220	7	2.5	312	2	AF2600	hypothetical prote
148	7	2.5	249	2	AF3225	hypothetical prote	221	7	2.5	312	2	AC0147	probable ABC trans
149	7	2.5	251	2	D85798	hypothetical prote	222	7	2.5	313	2	E70871	hypothetical prote
150	7	2.5	251	2	AH0742	high-affinity zinc	223	7	2.5	314	2	A39374	Renilla-luciferin
151	7	2.5	251	2	H75586	probable urea/short	224	7	2.5	314	2	B75076	daunorubicin resis
152	7	2.5	251	2	H90949	probable ABC trans	225	7	2.5	314	2	C87667	ABC transporter, A
153	7	2.5	251	2	B64948	probable ABC trans	226	7	2.5	315	2	F90396	conserved hypothet
154	7	2.5	253	2	H89795	hypothetical prote	227	7	2.5	315	2	A82655	phage-related prot
155	7	2.5	253	2	AD0251	high-affinity zinc	228	7	2.5	315	2	AI0777	ABC transporter At
156	7	2.5	254	2	G72687	probable high-affi	229	7	2.5	315	2	S72783	probable ABC-type
157	7	2.5	255	2	G90403	conserved hypothet	230	7	2.5	316	2	B90282	hypothetical prote
158	7	2.5	255	2	C89936	hypothetical prote	231	7	2.5	316	2	S19389	hypothetical prote
159	7	2.5	255	2	F70501	probable ABC-type	232	7	2.5	318	2	S70973	hlpf protein - Esc
160	7	2.5	257	2	B64458	high-affinity bran	233	7	2.5	319	2	E86861	methionyl-tRNA for
161	7	2.5	258	2	H84204	copper transport A	234	7	2.5	319	2	B53290	oligopeptide trans
162	7	2.5	260	2	T15237	hypothetical prote	235	7	2.5	320	2	S18444	G protein-coupled
163	7	2.5	260	2	B71234	probable transporter	236	7	2.5	323	2	F75202	dipeptide abc tran
164	7	2.5	261	2	E69159	hypothetical prote	237	7	2.5	324	2	G89934	hypothetical prote
165	7	2.5	261	2	AB3952	hypothetical prote	238	7	2.5	324	2	T35090	probable ABC trans
166	7	2.5	261	2	C98331	probable peptide A	239	7	2.5	328	2	G64901	ABC-type transport
167	7	2.5	264	2	AC2904	hypothetical prote	240	7	2.5	328	2	A85728	hypothetical prote
168	7	2.5	264	2	G97679	probable ATP-bindi	241	7	2.5	328	2	H90889	hypothetical prote
169	7	2.5	266	2	B97686	regulator protein	242	7	2.5	330	2	F72428	oligopeptide ABC t
170	7	2.5	266	2	AD2911	transcription regu	243	7	2.5	331	2	C72424	oligopeptide ABC t
171	7	2.5	266	2	A72401	ABC transporter, A	244	7	2.5	333	2	AC1209	teichoic acid tran
172	7	2.5	268	2	B64066	probable ABC trans	245	7	2.5	334	2	C87272	ABC transporter, A
173	7	2.5	269	2	A99919	hypothetical prote	246	7	2.5	335	2	AF1565	teichoic acid tran
174	7	2.5	274	2	H64219	hemolysin secretio	247	7	2.5	335	2	A82354	ATP-binding protei
175	7	2.5	274	2	S62815	sulfate transport	248	7	2.5	339	2	A82102	ABC transporter AT

249	7	2.5	339	2	A13609	daunorubicin resis	322	7	2.5	497	2	C34469	pule protein - K1e
250	7	2.5	340	2	T47019	hypothetical prote	323	7	2.5	498	2	S32859	outE protein - Brw
251	7	2.5	341	2	AF0236	probable glucamina	324	7	2.5	501	2	T00213	type II secretion
252	7	2.5	342	2	E65080	hypothetical prote	325	7	2.5	501	2	S22669	hypothetical prote
253	7	2.5	341	2	B91107	probable protein t	326	7	2.5	502	2	J00147	general secretion
254	7	2.5	341	2	E85952	probable protein t	327	7	2.5	503	2	JN0524	tepr protein - Vib
255	7	2.5	343	2	A10131	ABC transporter At	328	7	2.5	503	2	F82275	toxin co-regulated
256	7	2.5	343	2	A95224	ABC transporter A	329	7	2.5	503	2	AE0100	general secretion
257	7	2.5	343	2	D98088	hypothetical prote	330	7	2.5	513	2	C95089	ABC transporter, A
258	7	2.5	344	2	H82656	hypothetical prote	331	7	2.5	513	2	F97956	ABC transporter, A
259	7	2.5	344	2	JN0055	twitching motility	332	7	2.5	518	2	D89813	probable type II p
260	7	2.5	345	2	F82321	twitching motility	333	7	2.5	519	2	D81293	vga protein - Stap
261	7	2.5	346	2	G86262	hypothetical prote	334	7	2.5	522	2	JC1204	hypothetical prote
262	7	2.5	347	2	B81243	twitching motility	335	7	2.5	523	2	S61017	histidine ammonia-
263	7	2.5	347	2	C82016	probable pilus ret	336	7	2.5	524	2	F75610	58K protein - barl
264	7	2.5	351	2	S74729	carboxysome format	337	7	2.5	528	1	WMBV88	ABC transporter, A
265	7	2.5	352	2	T24154	hypothetical prote	338	7	2.5	533	2	E84626	probable ABC trans
266	7	2.5	352	2	E97108	pilr ATPase involv	339	7	2.5	533	2	H71886	bfpD protein - Esc
267	7	2.5	353	2	JC7661	G protein alpha su	340	7	2.5	534	2	S70971	hypothetical prote
268	7	2.5	353	2	S71965	GTP-binding regula	341	7	2.5	535	2	D90077	GCN20-2 protein -
269	7	2.5	353	2	T50482	G protein alpha ch	342	7	2.5	535	2	S56147	probable ABC trans
270	7	2.5	353	2	S46245	hypothetical prote	343	7	2.5	540	2	A95264	hypothetical prote
271	7	2.5	354	2	S46245	RAE-30 protein - m	344	7	2.5	540	2	AH3032	ABC transporter, A
272	7	2.5	354	2	S74323	ABC-type transport	345	7	2.5	542	2	H87373	conserved hypothet
273	7	2.5	355	2	T50479	G protein alpha ch	346	7	2.5	546	2	B87425	probable ABC trans
274	7	2.5	358	2	AD0115	conserved hypothet	347	7	2.5	547	2	T35267	endopeptidase IV-r
275	7	2.5	359	2	B70534	probable ribonucle	348	7	2.5	556	2	F75315	ABC transporter, A
276	7	2.5	360	2	C72263	motility protein P	349	7	2.5	560	2	F97925	hypothetical prote
277	7	2.5	361	2	T12470	hypothetical prote	350	7	2.5	560	2	A72329	general secretion
278	7	2.5	366	2	C70365	twitching motility	351	7	2.5	566	2	S28068	mxid protein - Shi
279	7	2.5	368	2	G82321	twitching motility	352	7	2.5	567	2	D98253	hypothetical prote
280	7	2.5	370	1	A63196	homoserine O-acety	353	7	2.5	571	2	H82355	peptide ABC transp
281	7	2.5	370	2	C82553	twitching motility	354	7	2.5	571	2	AH1418	ABC transporter, A
282	7	2.5	370	2	F70484	probable pilus ret	355	7	2.5	573	2	AH1793	ABC transporter, A
283	7	2.5	370	2	B81945	twitching motility	356	7	2.5	573	2	E69802	ABC transporter, A
284	7	2.5	370	2	B81945	arabinose ABC tran	357	7	2.5	573	2	A82231	transport ATP-bind
285	7	2.5	371	2	B90489	pilr protein - Nei	358	7	2.5	574	2	T27100	hypothetical prote
286	7	2.5	374	2	S32916	dipeptide transpor	359	7	2.5	575	2	C83313	probable type II s
287	7	2.5	376	2	AC3535	twitching motility	360	7	2.5	575	2	D84146	ABC transporter re
288	7	2.5	376	2	G82656	twitching motility	361	7	2.5	575	2	JC4554	ATP-binding caset
289	7	2.5	377	1	MFN285	matrix protein - s	362	7	2.5	575	2	D89834	MDR-type ABC trans
290	7	2.5	377	2	S74628	hypothetical prote	363	7	2.5	575	2	A97239	proteinase SM tran
291	7	2.5	383	1	A87049	probable phosphoes	364	7	2.5	576	2	A49933	ABC transporter, A
292	7	2.5	386	2	S68016	ATPase/RNA helicase	365	7	2.5	577	2	E72396	ABC transporter, A
293	7	2.5	399	2	B82723	carbamoyl-phosphat	366	7	2.5	577	2	C72275	phosphate response
294	7	2.5	403	1	C69213	protein-export mem	367	7	2.5	579	2	A27650	ABC transporter, A
295	7	2.5	403	2	F72254	hypothetical prote	368	7	2.5	580	2	AE1452	probable transport
296	7	2.5	408	2	A81243	twitching motility	369	7	2.5	582	2	AF0614	hypothetical prote
297	7	2.5	408	2	D82016	pilr-like protein	370	7	2.5	582	2	E90753	ATP-binding transp
298	7	2.5	420	2	B75333	twitching motility	371	7	2.5	582	2	S27998	probable ABC-type
299	7	2.5	421	2	AB2959	exopolysaccharide	372	7	2.5	582	2	C85617	ATP-binding transp
300	7	2.5	423	2	D98324	human N-acetylgluc	373	7	2.5	582	2	D82146	transport ATP-bind
301	7	2.5	427	2	AC1394	weakly human N-ace	374	7	2.5	584	2	AE0170	probable transport
302	7	2.5	427	2	AF1769	hypothetical prote	375	7	2.5	584	2	E97303	hypothetical prote
303	7	2.5	428	2	S76184	twitching motility	376	7	2.5	584	2	D87048	ABC-type transport
304	7	2.5	432	2	AB2222	ATP-binding protei	377	7	2.5	586	2	T48672	ATP-binding protei
305	7	2.5	437	2	T18555	thymidine phosphor	378	7	2.5	586	2	AH2133	hypothetical prote
306	7	2.5	438	2	AG2592	thymidine phosphor	379	7	2.5	587	2	F90044	hypothetical prote
307	7	2.5	438	2	A97375	probable MFS trans	380	7	2.5	587	2	AD3122	probable ABC trans
308	7	2.5	446	2	B83033	transcription regu	381	7	2.5	587	2	C98165	probable ABC trans
309	7	2.5	448	2	H70320	UDP-N-acetylmurama	382	7	2.5	587	2	H64045	probable ABC trans
310	7	2.5	451	2	A83145	probable transport	383	7	2.5	588	2	AI0381	moab protein limpo
311	7	2.5	452	2	AD0300	site-specific DNA-	384	7	2.5	588	2	T45539	hypothetical prote
312	7	2.5	452	2	S07886	probable peroxidase	385	7	2.5	589	2	H84985	probable ABC trans
313	7	2.5	460	2	D75610	cobryic acid synth	386	7	2.5	589	2	AH0559	ABC-type transport
314	7	2.5	465	2	H90508	DNA transfer prote	387	7	2.5	590	2	H64774	ATP-binding compon
315	7	2.5	475	2	D71871	transport protein	388	7	2.5	590	2	F90691	ATP-binding compon
316	7	2.5	481	2	S47441	hypothetical prote	389	7	2.5	590	2	B85542	ABC-type transport
317	7	2.5	490	2	G85354	general secretion	390	7	2.5	590	2	S75352	ATP-binding protei
318	7	2.5	491	2	E97159	shikimate kinase/3	391	7	2.5	593	2	AD2074	hypothetical prote
319	7	2.5	492	2	B72389	probable general s	392	7	2.5	597	2	T05329	
320	7	2.5	493	2	A65126	NADH2 dehydrogenas	393	7	2.5	598	2		
321	7	2.5	495	2	T11228		394	7	2.5				

395	7	2.5	598	2	T24717	hypothenical prote	468	7	2.5	1196	2	S65245	translation elonga
396	7	2.5	599	2	G83941	ABC transporter (A	469	7	2.5	1215	2	S65245	autoantigen - huma
397	7	2.5	600	2	B83875	two-component sens	470	7	2.5	1238	2	T18940	multidrug resistanc
398	7	2.5	603	2	AD2397	ATP-binding protei	471	7	2.5	1245	2	G86404	probable P-glycopr
399	7	2.5	604	2	A69858	ABC transporter (A	472	7	2.5	1247	2	F86405	probable P-glycopr
400	7	2.5	604	2	G95281	probable ABC trans	473	7	2.5	1269	2	S35366	furin (EC 3.4.21.7
401	7	2.5	606	2	T29190	hypothenical prote	474	7	2.5	1283	2	T18939	hypothenical prote
402	7	2.5	606	2	C88174	hypothenical ABC t	475	7	2.5	1307	2	T30882	multidrug resistanc
403	7	2.5	606	2	AB3113	hypothenical prote	476	7	2.5	1327	2	T41647	probable pre-mrna
404	7	2.5	609	2	AF2379	protease IV [imp	477	7	2.5	1345	2	A87102	probable SpoIIIE-f
405	7	2.5	609	2	E96742	probable ABC trans	478	7	2.5	1355	2	T00961	hypothenical prote
406	7	2.5	609	2	AB1245	D-1-deoxyxylulose	479	7	2.5	1362	2	T41534	leptomycin B resis
407	7	2.5	613	2	AD0796	NADH2 dehydrogenas	480	7	2.5	1407	1	T00558	probable ABC trans
408	7	2.5	614	2	D84630	hypothenical prote	481	7	2.5	1408	2	T47671	P-glycoprotein-li
409	7	2.5	614	2	B71884	hypothenical prote	482	7	2.5	1419	1	DVZQF	multidrug resistanc
410	7	2.5	619	2	T17193	probable protoporp	483	7	2.5	1427	2	T39219	hypothenical prote
411	7	2.5	620	1	I39755	adenyl-sulfate k	484	7	2.5	1431	2	T22748	hypothenical prote
412	7	2.5	622	2	T53777	hypothenical prote	485	7	2.5	1435	2	S59384	hypothenical prote
413	7	2.5	623	2	P69093	RNase L inhibitor	486	7	2.5	1447	2	T15200	hypothenical prote
414	7	2.5	630	2	D97669	hypothenical prote	487	7	2.5	1450	2	JC6139	cystic fibrosis tr
415	7	2.5	630	2	A12893	hypothenical prote	488	7	2.5	1451	2	T30821	P-glycoprotein - S
416	7	2.5	630	2	D95937	probable mureinpep	489	7	2.5	1469	2	T50210	probable ABC trans
417	7	2.5	632	2	A11607	D-1-deoxyxylulose	490	7	2.5	1472	2	B54774	ATP binding cassat
418	7	2.5	632	2	F97270	ATPase component o	491	7	2.5	1476	1	A39901	cystic fibrosis tr
419	7	2.5	633	2	H85932	probable adenyl-s	492	7	2.5	1476	1	A40303	cystic fibrosis tr
420	7	2.5	633	2	E97999	hypothenical prote	493	7	2.5	1480	1	DVHUCF	cystic fibrosis tr
421	7	2.5	633	2	H95128	ABC transporter, A	494	7	2.5	1481	1	A39323	cystic fibrosis tr
422	7	2.5	635	2	F86757	ABC transporter, A	495	7	2.5	1485	2	S23756	CFTFR protein - Afr
423	7	2.5	639	2	G82194	ABC transporter, A	496	7	2.5	1490	2	T47840	multi resistance p
424	7	2.5	640	2	H83267	probable ATP-bindi	497	7	2.5	1514	2	T52080	multi resistance p
425	7	2.5	641	1	Z228N0	adenyl-sulfate k	498	7	2.5	1515	2	T52081	MRP-like ABC trans
426	7	2.5	641	2	E95320	adenyl-sulfate k	499	7	2.5	1516	2	P84919	glutathione-conjug
427	7	2.5	641	2	F81408	ABC-type transmem	500	7	2.5	1529	2	A59189	ATP-binding cassat
428	7	2.5	651	2	A83230	hydantoin utilizat	501	7	2.5	1534	2	T30295	P-glycoprotein - T
429	7	2.5	656	2	S30483	pol polyprotein -	502	7	2.5	1539	2	T48059	ABC transporter-li
430	7	2.5	660	2	F98020	hypothenical prote	503	7	2.5	1548	1	DVLNS	multidrug resistanc
431	7	2.5	672	2	T43374	general secretion	504	7	2.5	1564	2	T27121	hypothenical prote
432	7	2.5	692	2	T03377	homeotic protein H	505	7	2.5	1576	2	S65774	homeotic protein H
433	7	2.5	695	2	S51433	MDL1 protein - yea	506	7	2.5	1677	2	T18344	P-glycoprotein E
434	7	2.5	705	2	B75371	ABC transporter, A	507	7	2.5	1704	2	T42749	ATP-binding cassat
435	7	2.5	708	2	C86404	probable protein A	508	7	2.5	1724	2	T18343	P-glycoprotein - S
436	7	2.5	712	2	S19387	saccharolysin (EC	509	7	2.5	1751	2	T50002	hypothenical prote
437	7	2.5	712	2	AG2058	ABC transporter AT	510	7	2.5	1758	2	P88559	protein C48B4.4b [
438	7	2.5	719	2	S62466	probable ATP-depen	511	7	2.5	1767	2	S60124	transport protein
439	7	2.5	727	2	F82634	cell-specific prot	512	7	2.5	2201	2	A54774	ATP binding cassat
440	7	2.5	733	2	T22813	hypothenical prote	513	7	2.5	2269	2	T18472	hypothenical prote
441	7	2.5	735	2	S37903	probable ATP-depen	514	7	2.5	2322	2	T10542	hypothenical prote
442	7	2.5	742	2	T20969	hypothenical prote	515	7	2.5	2672	2	A48126	translation activa
443	7	2.5	747	2	S35546	ATP-dependent RNA	516	7	2.5	2970	2	T08839	polyprotein - marm
444	7	2.5	752	2	S56146	GCN20 protein - ye	517	7	2.5	3005	2	T08841	polyprotein - dour
445	7	2.5	757	2	B75437	ABC transporter, A	518	7	2.5	3010	1	A45573	genome polyprotein
446	7	2.5	781	2	A85035	hypothenical prote	519	7	2.5	3010	1	GNWVCU	genome polyprotein
447	7	2.5	787	2	E71984	DNA transfer prote	520	7	2.5	3011	1	GNWVTC	genome polyprotein
448	7	2.5	787	2	A64522	virB4 homolog - He	521	7	2.5	3010	1	GNWVTW	genome polyprotein
449	7	2.5	790	1	S77032	ABC transporter sl	522	7	2.5	3010	1	S18030	genome polyprotein
450	7	2.5	798	2	S34023	TATA box-binding p	523	7	2.5	3011	1	GNWVC3	genome polyprotein
451	7	2.5	822	2	AD3232	conjugal transfer	524	7	2.5	3011	1	GNWVCH	genome polyprotein
452	7	2.5	832	2	B87673	ABC transporter, H	525	7	2.5	3011	1	S40770	genome polyprotein
453	7	2.5	863	2	C90482	ABC transporter, A	526	7	2.5	3014	1	JC5620	genome polyprotein
454	7	2.5	923	2	H64081	ATP-dependent heli	527	7	2.5	3033	1	GNWVJ8	genome polyprotein
455	7	2.5	932	2	H70929	hypothenical prote	528	7	2.5	3033	1	J01303	genome polyprotein
456	7	2.5	938	2	T05533	hypothenical prote	529	7	2.5	4131	2	T21085	hypothenical prote
457	7	2.5	945	2	JN0901	endopeptidase Clp	530	6	2.2	13	2	S09018	hemolytic protein
458	7	2.5	962	1	JT0669	helicase II-like p	531	6	2.2	24	2	S56000	guanine kinase M
459	7	2.5	1019	2	T29623	hypothenical prote	532	6	2.2	28	2	S16228	gene Bta protein
460	7	2.5	1025	2	T31014	hypothenical prote	533	6	2.2	28	2	I46921	aryl acylamidase -
461	7	2.5	1025	2	T18376	hypothenical prote	534	6	2.2	44	2	G69861	conserved hypothet
462	7	2.5	1034	2	T30331	multidrug resistanc	535	6	2.2	50	2	S61922	gene bap1(3) prote
463	7	2.5	1037	2	T50518	P-glycoprotein - T	536	6	2.2	55	2	UJ0359	hypothetical prote
464	7	2.5	1057	2	T38694	ABC transporter-li	537	6	2.2	56	2	T70665	MHC HLA-A24 cell s
465	7	2.5	1085	2	G89056	probable translati	538	6	2.2	58	2	E36491	phosphoprotein pho
466	7	2.5	1165	2	D72496	hypothenical prote	539	6	2.2	58	2	G36491	phosphoprotein pho
467	7	2.5	1194	1	G70837	probable ABC trans	540	6	2.2	58	2	C87333	hypothetical prote

541	6	2.2	66	2	S03443	dnak-type molecule	614	6	2.2	143	2	AD1693	hypothetical prote
542	6	2.2	75	2	T08508	trbK protein - Ent	615	6	2.2	144	2	G70894	hypothetical prote
543	6	2.2	75	2	S59102	hypothetical prote	616	6	2.2	145	2	AE1399	ribosomal protein
544	6	2.2	75	2	A97799	hypothetical prote	617	6	2.2	145	2	AD1775	ribosomal protein
545	6	2.2	76	2	S26642	replication licens	618	6	2.2	146	1	CUNLBF	blue copper protei
546	6	2.2	77	2	H91094	hypothetical prote	619	6	2.2	146	2	TS1473	calmodulin-like pr
547	6	2.2	77	2	A86399	protein F17L21.12	620	6	2.2	146	2	F70845	hypothetical prote
548	6	2.2	77	2	D85940	hypothetical prote	621	6	2.2	146	2	AF2642	conserved hypotet
549	6	2.2	78	2	S52172	replication licens	622	6	2.2	148	2	C82799	single-stranded DN
550	6	2.2	80	2	F83997	exodeoxyribonuclea	623	6	2.2	148	2	B88933	ribosomal protein
551	6	2.2	80	2	F86027	hypothetical prote	624	6	2.2	148	2	AE1594	hypothetical prote
552	6	2.2	80	2	AE2529	hypothetical prote	625	6	2.2	148	2	HT1007	hypothetical prote
553	6	2.2	82	2	AG0713	probable membrane	626	6	2.2	149	2	B69653	transcription regu
554	6	2.2	82	2	C64940	transglycosylase-a	627	6	2.2	149	2	D82178	hypothetical prote
555	6	2.2	82	2	D85790	transglycosylase-a	628	6	2.2	151	2	H82654	single-stranded DN
556	6	2.2	82	2	H90941	transglycosylase-a	629	6	2.2	152	2	F64441	molybdenum cofacto
557	6	2.2	82	2	JT0765	rapid lysis III pr	630	6	2.2	152	2	AC0286	conserved hypotet
558	6	2.2	86	2	E95225	hypothetical prote	631	6	2.2	154	2	H69376	hypothetical prote
559	6	2.2	86	2	H98089	hypothetical prote	632	6	2.2	154	2	T04159	histone H1 homolog
560	6	2.2	88	2	H86752	prophage p12 prote	633	6	2.2	155	2	F45831	MHC class I histoc
561	6	2.2	89	2	D83052	30S ribosomal prot	634	6	2.2	155	2	S70046	hypothetical prote
562	6	2.2	90	2	T04077	probable ribosomal	635	6	2.2	155	2	T21364	hypothetical prote
563	6	2.2	90	2	AD1606	hypothetical prote	636	6	2.2	156	2	E84991	30S ribosomal prot
564	6	2.2	90	2	AH1243	hypothetical prote	637	6	2.2	156	2	C86626	hypothetical prote
565	6	2.2	91	2	A46685	GTP-binding regula	638	6	2.2	157	2	G97424	hypothetical prote
566	6	2.2	93	2	AC0081	conserved hypotet	639	6	2.2	157	2	AC2405	conserved hypotet
567	6	2.2	94	2	E45831	MHC class I histoc	640	6	2.2	158	2	G70323	gene 60 protein -
568	6	2.2	96	2	G86801	prophage p13 prote	641	6	2.2	159	1	W2BE60	H+-transporting tw
569	6	2.2	100	2	F82453	conserved hypotet	642	6	2.2	159	2	S28959	probable molybdenu
570	6	2.2	106	2	A71193	hypothetical prote	643	6	2.2	159	2	C71192	molybdenum cofacto
571	6	2.2	107	2	AC0145	probable membrane	644	6	2.2	159	2	E75151	hypothetical prote
572	6	2.2	108	2	S67638	forkhead transcrip	645	6	2.2	160	2	C64353	hypothetical prote
573	6	2.2	108	2	A48924	forkhead transcrip	646	6	2.2	160	2	S77246	probable signal pe
574	6	2.2	110	2	B48924	ABC transporter, A	647	6	2.2	161	2	D90273	phosphohistidine p
575	6	2.2	110	2	AB1526	cobalt transport A	648	6	2.2	162	2	C64482	hypothetical prote
576	6	2.2	110	2	B85965	hypothetical prote	649	6	2.2	162	2	E90275	thermoresistant gl
577	6	2.2	111	2	F72267	hypothetical prote	650	6	2.2	162	2	E97382	glucosyltransferase
578	6	2.2	113	2	I73629	phosphoprotein pho	651	6	2.2	163	2	AD7382	glucosyltransferase
579	6	2.2	114	2	D36769	14R protein - huma	652	6	2.2	163	2	AD2600	photosystem I chai
580	6	2.2	114	2	C90344	hypothetical prote	653	6	2.2	164	2	S22204	shikimate kinase
581	6	2.2	115	2	D70123	ribosomal protein	654	6	2.2	164	2	AE1382	probable cdc2-like
582	6	2.2	115	2	S77435	hypothetical prote	655	6	2.2	165	2	A81382	stress related pro
583	6	2.2	115	2	F75284	hypothetical prote	656	6	2.2	166	2	T12201	thiol peroxidase
584	6	2.2	116	2	S16961	GTP-binding protei	657	6	2.2	167	2	T11750	ferritin [imported
585	6	2.2	116	2	H65091	hypothetical prote	658	6	2.2	168	2	AG0659	2',3'-cyclic-nucle
586	6	2.2	117	2	I57454	MHC class I antige	659	6	2.2	169	2	AE0217	Ig heavy chain V r
587	6	2.2	118	2	AC0891	conserved hypotet	660	6	2.2	171	2	S23623	hypothetical prote
588	6	2.2	118	2	AG1004	conserved hypotet	661	6	2.2	171	2	B71147	thermoresistant gl
589	6	2.2	118	2	T01246	30S ribosomal prot	662	6	2.2	172	2	B75338	transcription repr
590	6	2.2	118	2	B91120	hypothetical prote	663	6	2.2	173	2	B39141	conserved hypotet
591	6	2.2	119	2	S77748	probable ABC-type	664	6	2.2	174	1	G69008	modulates DNA topo
592	6	2.2	119	2	S77748	hydrogenase expres	665	6	2.2	174	2	C97964	hypothetical prote
593	6	2.2	120	2	A75586	hypothetical prote	666	6	2.2	175	2	F69745	hypothetical prote
594	6	2.2	120	2	A84778	lipid transfer pro	667	6	2.2	175	2	A64354	hypothetical prote
595	6	2.2	122	2	T05950	probable membrane	668	6	2.2	176	2	E97553	hypothetical prote
596	6	2.2	123	2	B97181	hypothetical prote	669	6	2.2	176	2	S37737	hypothetical prote
597	6	2.2	124	2	A70692	probable membrane	670	6	2.2	176	2	I41076	hypothetical prote
598	6	2.2	124	2	S67606	carboxymycin-resista	671	6	2.2	177	2	H86710	probable kinase fr
599	6	2.2	124	2	JC1181	Ig heavy chain V r	672	6	2.2	177	2	H97205	MHC class I histoc
600	6	2.2	125	2	S68170	hypothetical prote	673	6	2.2	178	2	C45831	hypothetical prote
601	6	2.2	126	2	S69804	translation initia	674	6	2.2	178	2	D64036	hypothetical prote
602	6	2.2	127	2	A75086	hypothetical prote	675	6	2.2	178	2	T03079	hypothetical prote
603	6	2.2	129	2	H97938	blastocidin-S deam	676	6	2.2	179	2	T30724	MHC class I histoc
604	6	2.2	130	2	S41571	hypothetical prote	677	6	2.2	180	2	D45831	suu ribosomal prot
605	6	2.2	130	2	E97737	hypothetical prote	678	6	2.2	180	2	C75171	ribosomal protein
606	6	2.2	131	2	B97737	conserved hypotet	679	6	2.2	180	2	D70161	hypothetical prote
607	6	2.2	133	2	AI2834	hypothetical 14.2K	680	6	2.2	181	2	S74491	adenylate kinase
608	6	2.2	134	2	D97612	transcription regu	681	6	2.2	181	2	F70105	hypothetical prote
609	6	2.2	135	2	D83795	conserved hypotet	682	6	2.2	181	2	D72468	hypothetical prote
610	6	2.2	140	2	B81121	hypothetical prote	683	6	2.2	181	2	T49759	related to microci
611	6	2.2	140	2	C64027	Ig heavy chain V r	684	6	2.2	181	2	T35851	hypothetical prote
612	6	2.2	142	2	A32483	hypothetical prote	685	6	2.2	181	2	AH2483	hypothetical prote
613	6	2.2	143	2	AC1322	hypothetical prote	686	6	2.2	181	2		

687	6	2.2	182	2	H71899	hypothetical prote	760	6	2.2	210	2	H83570	probable two-compo
688	6	2.2	183	2	AH1304	pyrimidine operon	761	6	2.2	210	2	AH0234	probable two-compo
689	6	2.2	183	2	AH1676	pyrimidine operon	762	6	2.2	210	2	T47033	hypothetical prote
690	6	2.2	183	2	AB3405	hypothetical prote	763	6	2.2	210	2	G95228	ABC transporter, A
691	6	2.2	184	2	AD1815	adenylate kinase (764	6	2.2	210	2	C98093	hypothetical prote
692	6	2.2	185	1	MOCH4E	myosin alkali ligh	765	6	2.2	212	2	G69369	branched-chain ami
693	6	2.2	185	2	S60778	dihydrodipicolinat	766	6	2.2	212	2	T03528	cob(I)alamin adeno
694	6	2.2	185	2	A70048	amino acid ABC tra	767	6	2.2	213	2	AF0408	adenyl-yl-sulfate k
695	6	2.2	185	2	AF2236	hypothetical prote	768	6	2.2	213	2	C64542	ABC transporter, A
696	6	2.2	186	2	S27735	hypothetical prote	769	6	2.2	213	2	C71965	ABC transporter, A
697	6	2.2	186	2	B72695	hypothetical prote	770	6	2.2	213	2	F97681	ABC-type transporter
698	6	2.2	186	2	T32408	hypothetical prote	771	6	2.2	213	2	AE2906	hypothetical prote
699	6	2.2	186	2	AB0132	conserved hypothet	772	6	2.2	213	2	F98019	hypothetical prote
700	6	2.2	188	2	AB3472	hypothetical prote	773	6	2.2	213	2	A95013	hypothetical prote
701	6	2.2	189	1	S74659	shikimate kinase (774	6	2.2	213	2	G95079	ABC transporter, A
702	6	2.2	189	2	S49558	hypothetical prote	775	6	2.2	213	2	T30618	hypothetical prote
703	6	2.2	190	2	JC6062	ribosomal protein	776	6	2.2	213	2	D97884	hypothetical prote
704	6	2.2	190	2	T03761	probable ribosomal	777	6	2.2	213	2	B97947	hypothetical prote
705	6	2.2	190	2	AD2386	hypothetical prote	778	6	2.2	214	1	S23663	hela protein - Rho
706	6	2.2	191	2	S51496	GTP-binding protei	779	6	2.2	214	2	A03309	dnak-type molecula
707	6	2.2	191	2	C64458	high-affinity bran	780	6	2.2	214	2	D86533	frame-shift with C
708	6	2.2	191	2	F86826	hypothetical prote	781	6	2.2	214	2	T14920	hypothetical prote
709	6	2.2	192	1	RSRT9	ribosomal protein	782	6	2.2	214	2	G72669	hypothetical prote
710	6	2.2	192	2	S65792	ribosomal protein	783	6	2.2	215	2	JC5483	ABC-type transporter
711	6	2.2	192	2	A84325	cytidylate kinase	784	6	2.2	215	2	C59767	conserved hypothet
712	6	2.2	192	2	AH0557	probable lipoprote	785	6	2.2	215	2	H90141	conserved hypothet
713	6	2.2	193	1	MOMS4E	myosin alkali ligh	786	6	2.2	215	2	B84078	hypothetical prote
714	6	2.2	193	1	MORT4E	myosin alkali ligh	787	6	2.2	216	2	B70317	H+-transporting tw
715	6	2.2	193	2	AG1323	3-isopropylmalate	788	6	2.2	216	2	H71892	osmoprotection ATP
716	6	2.2	193	2	AG1694	probable translati	789	6	2.2	216	2	C64622	osmoprotection pro
717	6	2.2	193	2	T14618	conserved hypothet	790	6	2.2	216	2	B82020	ABC transporter AT
718	6	2.2	193	2	C90469	conserved hypothet	791	6	2.2	216	2	T34527	hypothetical prote
719	6	2.2	194	1	MOCHLC	myosin alkali ligh	792	6	2.2	217	2	D81263	probable ABC trans
720	6	2.2	194	2	F69985	transcription regu	793	6	2.2	217	2	T33043	hypothetical prote
721	6	2.2	194	2	C98147	frck protein (AF19	794	6	2.2	218	2	C97236	ABC transporter, A
722	6	2.2	194	2	G71038	hypothetical prote	795	6	2.2	218	2	S76385	hypothetical prote
723	6	2.2	195	1	MOH03V	myosin alkali ligh	796	6	2.2	218	2	AB0876	probable ABC-trans
724	6	2.2	195	2	A82416	conserved hypothet	797	6	2.2	218	2	H64644	PARA protein - Hel
725	6	2.2	195	2	T24033	hypothetical prote	798	6	2.2	218	2	AD2019	cell-division ATP-
726	6	2.2	197	1	MOH04E	myosin alkali ligh	799	6	2.2	218	2	G71197	hypothetical prote
727	6	2.2	197	2	E72294	thymidylate kinase	800	6	2.2	219	2	A70338	ABC transporters (
728	6	2.2	198	2	JQ0864	hypothetical 21.9K	801	6	2.2	219	2	AD1471	ABC transporter
729	6	2.2	199	2	F81307	probable integral	802	6	2.2	219	2	AE3215	hypothetical prote
730	6	2.2	200	1	MORT3V	myosin alkali ligh	803	6	2.2	220	2	E75090	adenylate kinase (
731	6	2.2	200	2	E69912	adenylsulfate ki	804	6	2.2	220	2	G89132	ABC transporter (g
732	6	2.2	201	1	B65056	adenyl-yl-sulfate k	805	6	2.2	220	2	H71360	probable thiamin A
733	6	2.2	201	2	AH0856	adenosine 5'-phosp	806	6	2.2	220	2	H72252	conserved hypothet
734	6	2.2	201	2	D91079	adenosine 5'-phosp	807	6	2.2	220	2	AI3140	cytidylate kinase
735	6	2.2	201	2	E85924	adenosine 5'-phosp	808	6	2.2	220	2	G90194	conserved hypothet
736	6	2.2	201	2	H82055	peptidyl-prolyl ci	809	6	2.2	220	2	G90047	hypothetical prote
737	6	2.2	202	1	S17244	adenyl-yl-sulfate k	810	6	2.2	220	2	AF1561	ABC transporter, A
738	6	2.2	202	2	T50101	adenylsulfate ki	811	6	2.2	220	2	AG1204	ABC transporter, A
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740	6	2.2	202	2	B90180	ABC transporter, A	813	6	2.2	221	2	G81335	probable ABC trans
741	6	2.2	203	2	E83166	hypothetical prote	814	6	2.2	221	2	AF1862	ATP-binding protei
742	6	2.2	204	2	D95394	probable transcrip	815	6	2.2	221	2	B84160	amino acid ABC tra
743	6	2.2	205	2	T10296	fibroblast growth	816	6	2.2	221	2	F69369	branched-chain ami
744	6	2.2	205	2	F87660	hydrolase, haloaci	817	6	2.2	221	2	E78834	ABC transporter AT
745	6	2.2	205	2	T04918	hypothetical prote	818	6	2.2	221	2	F71676	glutamine transpor
746	6	2.2	206	2	A84236	30S ribosomal prot	819	6	2.2	222	2	AD1137	ribulose-5-phospha
747	6	2.2	206	2	AC0520	conserved hypothet	820	6	2.2	222	2	AC1495	hypothetical prote
748	6	2.2	206	2	C85493	probable DNA repai	821	6	2.2	222	2	AF3133	H+-exporting ATPas
749	6	2.2	206	2	G90642	probable DNA repai	822	6	2.2	222	2	S25014	hypothetical prote
750	6	2.2	206	2	G64732	yacE protein - Esc	823	6	2.2	222	2	C96992	hypothetical prote
751	6	2.2	206	2	AH0416	conserved hypothet	824	6	2.2	222	2	T34753	probable ATP/GTP b
752	6	2.2	206	2	AE5331	probable cytochrom	825	6	2.2	222	2	AE0182	ABC transporter AT
753	6	2.2	207	2	T21903	hypothetical prote	826	6	2.2	223	2	D64613	cell division prot
754	6	2.2	207	2	F75535	deoxyguanosine kin	827	6	2.2	223	2	E71900	probable ABC trans
755	6	2.2	207	2	AI0002	secreted thiol,dis	828	6	2.2	223	2	E83596	DNA mismatch repai
756	6	2.2	207	2	G95864	probable ABC trans	829	6	2.2	223	2	C86707	ABC transporter AT
757	6	2.2	207	2	B82480	transcription regu	830	6	2.2	223	2	H86906	ABC transporter AT
758	6	2.2	208	2	B44261	dnak-type molecula	831	6	2.2	223	2	D83869	ABC transporter (A
759	6	2.2	209	2	T29196	hypothetical prote	832	6	2.2	223	2	B83697	hypothetical prote

833	6	2.2	223	2	B97178	ABC transporter, A	906	6	2.2	231	2	C69317	conserved hypothe
834	6	2.2	223	2	S74812	ABC-type transport	907	6	2.2	231	2	B86154	T6A9.7 protein - A
835	6	2.2	224	2	A41485	ABC transporter, A	908	6	2.2	231	2	C70000	ABC transporter (A
836	6	2.2	224	2	C82903	cytidylate kinase	909	6	2.2	231	2	C81909	probable ABC-trans
837	6	2.2	224	2	T43331	clathrin light cha	910	6	2.2	232	2	B83922	ABC transporter, A
838	6	2.2	224	2	H72346	basal-body rod mod	911	6	2.2	232	2	B84728	probable ABC-type
839	6	2.2	224	2	H72046	conserved hypothe	912	6	2.2	232	2	F85488	hypothetical prote
840	6	2.2	224	2	A86579	CT668 hypothetical	913	6	2.2	232	2	F90637	hypothetical prote
841	6	2.2	224	2	B97146	ABC-type transport	914	6	2.2	232	2	A11946	hypothetical prote
842	6	2.2	224	2	B70327	ABC transporter -	915	6	2.2	232	2	G84382	cobalt transporter A
843	6	2.2	225	2	A36459	orotate phosphorib	916	6	2.2	232	2	C97089	ABC transporter, A
844	6	2.2	225	2	E90260	ABC transporter, A	917	6	2.2	232	2	C70355	ABC transporter, A
845	6	2.2	225	2	B91104	probable ABC trans	918	6	2.2	232	2	C69822	glycine betaine/L-
846	6	2.2	225	2	B85949	probable ABC trans	919	6	2.2	233	2	B90210	hypothetical prote
847	6	2.2	225	2	AH1294	hypothetical prote	920	6	2.2	233	2	D96763	hypothetical prote
848	6	2.2	225	2	F71439	probable serine pr	921	6	2.2	233	2	B95091	ABC transporter, A
849	6	2.2	225	2	F89795	hypothetical prote	922	6	2.2	233	2	C97558	hypothetical prote
850	6	2.2	225	2	A82374	ABC transporter AT	923	6	2.2	233	2	A97337	ABC-type transport
851	6	2.2	226	2	D69433	ABC transporter, A	924	6	2.2	233	2	A82184	ABC transporter, A
852	6	2.2	226	2	S75665	ABC-type transport	925	6	2.2	233	2	AF1994	ATP-binding protei
853	6	2.2	226	2	B75270	ABC transporter, A	926	6	2.2	233	2	JQ0097	hypothetical 26K p
854	6	2.2	226	2	A97340	ABC-type transport	927	6	2.2	233	2	D28356	hypothetical prote
855	6	2.2	226	2	D35719	hisp-like nucleoti	928	6	2.2	233	2	D97118	RNA polymerase sig
856	6	2.2	226	2	D86104	ATP-binding compon	929	6	2.2	233	2	AC0645	ABC transporter AT
857	6	2.2	226	2	G91263	ATP-binding compon	930	6	2.2	234	2	H72385	ABC transporter, A
858	6	2.2	226	2	S60562	H+-transporting tw	931	6	2.2	234	2	T37141	probable membrane
859	6	2.2	226	2	A31335	H+-exporting ATPas	932	6	2.2	234	2	A70736	hypothetical prote
860	6	2.2	226	2	T34827	probable potassium	933	6	2.2	234	2	H87364	ABC transporter, A
861	6	2.2	226	2	A12774	ribose 5-phosphate	934	6	2.2	234	2	H69253	conserved hypothe
862	6	2.2	226	2	B89782	hypothetical prote	935	6	2.2	234	2	D96932	ABC transporter, A
863	6	2.2	226	2	AB1741	ABC-transporter AT	936	6	2.2	234	2	AF0198	lipoprotein releas
864	6	2.2	226	2	AD1371	ABC transporter, A	937	6	2.2	234	2	AC1094	high-affinity zinc
865	6	2.2	226	2	C71307	probable ABC trans	938	6	2.2	234	2	A11456	high-affinity zinc
866	6	2.2	227	2	A75304	ABC transporter, A	939	6	2.2	235	1	AB2613	25K protein - whit
867	6	2.2	227	2	B84040	ABC transporter (A	940	6	2.2	235	2	AB2613	monop
868	6	2.2	227	2	A84109	ABC transporter (A	941	6	2.2	235	2	I68700	MHC HLA-A cell sur
869	6	2.2	227	2	A64129	probable ABC-type	942	6	2.2	235	2	S60887	ferric exochelin u
870	6	2.2	227	2	AI0875	probable ABC-trans	943	6	2.2	235	2	AG0515	hypothetical ABC t
871	6	2.2	227	2	B83288	probable ATP-bindi	944	6	2.2	235	2	D64399	glutamine transpor
872	6	2.2	227	2	D83271	probable ATP-bindi	945	6	2.2	235	2	G71259	probable ABC trans
873	6	2.2	227	2	B82177	ABC transporter, A	946	6	2.2	235	2	D90790	probable ATP bindi
874	6	2.2	227	2	B82408	ABC transporter, A	947	6	2.2	235	2	G85650	probable ATP bindi
875	6	2.2	227	2	F96955	ABC transporter, A	948	6	2.2	235	2	T50170	hypothetical prote
876	6	2.2	227	2	F96364	ABC transporter, A	949	6	2.2	235	2	H96023	probable phosphon
877	6	2.2	228	2	AF0565	hypothetical ABC t	950	6	2.2	235	2	S63697	hypothetical prote
878	6	2.2	228	2	A96939	ABC transporter, A	951	6	2.2	235	2	AB2598	hypothetical prote
879	6	2.2	228	2	B69377	ABC transporter AT	952	6	2.2	235	2	G86519	ABC transport ATPa
880	6	2.2	228	2	F90698	probable ABC-type	953	6	2.2	235	2	D72102	ABC transporter, A
881	6	2.2	228	2	F64780	probable ABC-type	954	6	2.2	235	2	B72369	ABC transporter, A
882	6	2.2	228	2	H85548	probable ABC-trans	955	6	2.2	236	2	T07260	sulfate transport
883	6	2.2	228	2	AF0374	probable ABC trans	956	6	2.2	236	2	D69423	branched-chain ami
884	6	2.2	228	2	D83071	probable ATP-bindi	957	6	2.2	236	2	D90461	hypothetical prote
885	6	2.2	228	2	T37623	hypothetical prote	958	6	2.2	236	2	I39835	transcription acti
886	6	2.2	228	2	B64856	probable ABC-type	959	6	2.2	236	2	D84103	two-component resp
887	6	2.2	228	2	A75516	ABC transporter, A	960	6	2.2	236	2	S01086	hypothetical prote
888	6	2.2	228	2	G90815	hypothetical prote	961	6	2.2	236	2	D84103	hypothetical prote
889	6	2.2	228	2	C85675	hypothetical prote	962	6	2.2	236	2	AG2905	probable ATP-bindi
890	6	2.2	228	2	A82147	ABC transporter, A	963	6	2.2	236	2	H97680	ABC transporter UU
891	6	2.2	229	2	T45311	cell division atp-	964	6	2.2	236	2	F82934	probable ABC trans
892	6	2.2	229	2	E70919	cell division atp-	965	6	2.2	236	2	C71517	heme oxygenase [im
893	6	2.2	229	2	E96558	hypothetical prote	966	6	2.2	237	2	AF2196	probable ABC trans
894	6	2.2	229	2	T40789	clathrin light cha	967	6	2.2	237	2	F86789	manganese ABC tran
895	6	2.2	229	2	T40068	probable ABC-type	968	6	2.2	237	2	G65084	hypothetical prote
896	6	2.2	229	2	E70405	ABC transporter -	969	6	2.2	237	2	C83689	hypothetical prote
897	6	2.2	230	2	T28262	ORF MSV100 probabl	970	6	2.2	238	2	I68699	MHC HLA-A cell sur
898	6	2.2	230	2	AC1059	ABC transporter, A	971	6	2.2	238	2	AF0607	arginine transport
899	6	2.2	230	2	AB1462	ABC transporter, A	972	6	2.2	238	2	F64824	arginine 3rd trans
900	6	2.2	230	2	H65084	hypothetical prote	973	6	2.2	238	2	B85597	arginine 3rd trans
901	6	2.2	230	2	H97343	ABC transport syst	974	6	2.2	238	2	A90747	arginine transport
902	6	2.2	230	2	F83697	ABC transporter (A	975	6	2.2	238	2	AH0164	cobalt transport A
903	6	2.2	230	2	C71548	probable ABC trans	976	6	2.2	238	2	H69479	probable glutamine
904	6	2.2	231	2	C81107	ABC transporter, A	977	6	2.2	238	2	C72576	probable ATP-bindi
905	6	2.2	231	2	G97554	ribose 5-phosphate	978	6	2.2	238	2	A83224	

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979 6 2.2 238 2 AG2909
980 6 2.2 238 2 E71375
981 6 2.2 238 2 F75035
982 6 2.2 239 2 H97578
983 6 2.2 239 2 H97799
984 6 2.2 239 2 F82386
985 6 2.2 239 2 AG0420
986 6 2.2 239 2 E70800
987 6 2.2 239 2 S64324
988 6 2.2 239 2 AE1317
989 6 2.2 240 1 AR3CGO
990 6 2.2 240 2 AC3548
991 6 2.2 240 2 A10600
992 6 2.2 240 2 H69962
993 6 2.2 240 2 G83832
994 6 2.2 240 2 G90739
995 6 2.2 240 2 A85590
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ALIGNMENTS

RESULT 1
ABC transporter, ATP-binding protein SP2220 [imported] - Streptococcus pneumoniae (strain C95259)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 16-Aug-2004
C:Accession: C95259
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidon, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, non, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete Genome Sequence of a Virulent Isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: C95259
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-279 <KUR>
A:Cross-references: UNIPROT:Q97N51; GB:AE005672; PIDN:AAK76268.1; PID:g14973730; GSPDB:G
A:Experimental source: strain TIGR4
C:Gene: SP2220
C:Superfamily: ATP-binding cassette homology

Query Match 100.0%; Score 279; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 3.5e-271;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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F98124
hypothetical protein ABC-NBP [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 16-Aug-2004
C:Accession: F98124
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Ede, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; McKee, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: F98124
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-279 <KUR>
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C:Gene: ABC-NBP
C:Superfamily: ATP-binding cassette homology

Query Match 59.9%; Score 167; DB 2; Length 279;
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QY 72 TSTSKNKDRIQIRKQVGLVFOFAENQIFETVLKDVAFGPQNGFVGSBEDAVKTAREKIAL 131
DB 72 TSTSKNKDRIQIRKQVGLVFOFAENQIFETVLKDVAFGPQNGFVGSBEDAVKTAREKIAL 131
QY 132 VGIDESLPDRSPFELSGQMRVAIAGILAMEPAILVLDEPTAGLDPLGRKELMTLPKKL 191
DB 132 VGIDESLPDRSPFELSGQMRVAIAGILAMEPAILVLDEPTAGLDPLGRKELMTLPKKL 191
QY 192 HQSGMTIVLVTHLMDVVAEYANQYVMEKGLRVKGGKPSDVFDQVVFMEVQLGVPKITA 251
DB 192 HQSGMTIVLVTHLMDVVAEYANQYVMEKGLRVKGGKPSDVFDQVVFMEVQLGVPKITA 251
QY 252 FCKRLADRGVSFKRLPIKIEEFKESLNG 279
DB 252 FCKRLADRGVSFKRLPIKIEEFKESLNG 279

RESULT 3
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ABC transporter ATP-binding protein ychB [imported] - Lactococcus lactis subsp. lactis (C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 16-Aug-2004
C:Accession: F86659
R:Solotkin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssi
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: F86659
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <STO>
A:Cross-references: UNIPROT:Q9CIS8; GB:AE005176; PID:g12723140; PIDN:AAK04376.1; GSPDB:G
A:Experimental source: strain ILL1403
C:Gene: ychB
C:Superfamily: ATP-binding cassette homology

Query Match 8.2%; Score 23; DB 2; Length 288;
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Db 141 SPFFELSGGQMRRAVAIAAG 163

RESULT 4
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ABC transporter (ATP-binding protein) homolog ybaE - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
C:Accession: E69742
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Alvertini, A.M.; Allioni, G.; Azevedo, V.; Bertero,
C.; Bron, S.; Brouillet, C.V.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Fulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Puma, S.; Galizzi, A.; Gallen
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: E69742
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-276 <KUN>
A:Cross-references: UNIPROT:P70970; GB:Z99104; GB:AL009126; NID:G2632267; PIDN:CAB11922.
A:Experimental source: strain 168
C:Genetics:
A:Gene: ybaE
C:Superfamily: ATP-binding cassette homology
C:Keywords: ATP; nucleotide binding; P-loop
F:10-209/Domain: ATP-binding cassette homology <ABC>
F:27-34/Region: nucleotide-binding motif A (P-loop)

Query Match 6.8%; Score 19; DB 2; Length 276;
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 DRSPFELSGGQMRRAVAIAAG 158
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Db 127 DRSPFELSGGQMRRAVAIAAG 145

RESULT 5
AH1399
ABC transporter (ATP-binding protein) homolog lmo2600 [imported] - Listeria monocytogenes
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH1399
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1399
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <GLA>
A:Cross-references: UNIPROT:Q8Y455; GB:NC_003210; PIDN:CAD00678.1; PID:G16412088; GSPDB:
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo2600
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
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Query Match 6.5%; Score 18; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 8e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 RSPFELSGGQMRRAVAIAAG 158
|||||
Db 141 RSPFELSGGQMRRAVAIAAG 158

RESULT 6
AG1775
ABC transporter (ATP-binding protein) homolog lin2749 [imported] - Listeria innocua (str
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AG1775
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1775
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <GLA>
A:Cross-references: UNIPROT:Q927N9; GB:AL592022; PIDN:CAC97975.1; PID:G16415285; GSPDB:G
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lin2749
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 6.5%; Score 18; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 8e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 RSPFELSGGQMRRAVAIAAG 158
|||||
Db 141 RSPFELSGGQMRRAVAIAAG 158

RESULT 7
T44413
ABC transporter (ATP-binding protein) homolog ybaE [imported] - Bacillus halodurans
C:Species: Bacillus halodurans
C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C:Accession: T44413
R:Takami, H.; Takaki, Y.; Nakasone, K.; Hiram, C.; Inoue, A.; Horikoshi, K.
BioSci. Biotechnol. Biochem. 63, 452-455, 1999
A:Title: Sequence analysis of a 32-kb region including the major ribosomal protein gene
A:Reference number: Z22756; MUID:99209008; PMID:10192928
A:Accession: T44413
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-183 <TAK>
A:Cross-references: UNIPROT:Q929J2; EMBL:AB017508; NID:G4512395; PIDN:BAAY75301.1; PID:G4
A:Experimental source: strain C-125
C:Genetics:
A:Note: ybaE

Query Match 4.7%; Score 13; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 5.3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 LSGGQMRRAVAIAAG 158
|||||
Db 35 LSGGQMRRAVAIAAG 47

RESULT 8
E83670
ABC transporter (ATP-binding protein) BH0165 [imported] - Bacillus halodurans (strain C-
```

C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 16-Aug-2004
C:Accession: B83670
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: B83670
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-282 <STO>
A:Cross-references: UNIPROT:Q9KGD6; GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BA8038
A:Experimental source: strain C-125
C:Genetics:
C:Superfamily: ATP-binding cassette homology

Query Match 4.7%; Score 13; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 LSGGQRRVAIAG 158
|||||
DB 134 LSGGQRRVAIAG 146
|||||

RESULT 9
C90560
ABC transporter atp-binding protein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 16-Aug-2004
C:Accession: C90560
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A95512; MUID:21267165; PMID:11353084
A:Accession: C90560
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-304 <KUR>
A:Cross-references: UNIPROT:Q9OH4; GB:AL445566; PID:g14089801; PIDN:CAC13560.1; GSPDB:G
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPU 3870
A:Genetic code: SGC3
C:Superfamily: ATP-binding cassette homology

Query Match 4.3%; Score 12; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LVLDPTAGLDLP 178
|||||
DB 183 LVLDPTAGLDLP 194
|||||

RESULT 10
G72598
probable ABC transporter ATP-binding protein APE1255 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 16-Aug-2004
C:Accession: G72598
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: G72598
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-253 <RAW>
A:Cross-references: UNIPROT:Q9YCK2; DDBJ:AP000061; NID:g5104821; PIDN:BAA80245.1; PID:dl
A:Experimental source: strain K1

C:Genetics:
A:Gene: APE1255
C:Superfamily: ATP-binding cassette homology

Query Match 3.9%; Score 11; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 VLDEPTAGLDLP 178
|||||
DB 164 VLDEPTAGLDLP 174
|||||

RESULT 11
G64435
cobalt transport ATP-binding protein O homolog - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
C:Accession: G64435
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
reón, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: G64435
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-279 <BUL>
A:Cross-references: UNIPROT:Q58488; GB:U67551; GB:L77117; NID:g1591728; PIDN:AAB99089.1;
C:Genetics:
A:Map position: REV1027976-1027137
C:Superfamily: ATP-binding cassette homology
C:Keywords: ATP; nucleotide binding; P-loop
F:20-215/Domain: ATP-binding cassette homology <ABC>
F:37-44/Region: nucleotide-binding motif A (P-loop)

Query Match 3.9%; Score 11; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 0.008;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 VLDEPTAGLDLP 178
|||||
DB 162 VLDEPTAGLDLP 172
|||||

RESULT 12
S34187
probable ABC-type transport protein TnrB2 - Streptomyces longisporoflavus
C:Species: Streptomyces longisporoflavus
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-2004
C:Accession: S34187; S42415
R:Cooper, H.N.
submitted to the EMBL Data Library, June 1993
A:Reference number: S34187
A:Accession: S34187
A:Molecule type: DNA
A:Residues: 1-300 <COO>
A:Cross-references: UNIPROT:Q54406; EMBL:X73633; NID:g313336; PIDN:CAAS2012.1; PID:g5817
R:Linton, K.J.; Cooper, H.N.; Hunter, I.S.; Leadlay, P.F.
Mol. Microbiol. 11, 777-785, 1994
A:Title: An ABC-transporter from Streptomyces longisporoflavus confers resistance to the
A:Reference number: S42415; MUID:94254733; PMID:8196549
A:Accession: S42415
A:Molecule type: DNA
A:Residues: 14-53;123-162 <LIN>
A:Cross-references: EMBL:X73633
A:Experimental source: strain 83E6
C:Genetics:
A:Start codon: GTG
C:Superfamily: ATP-binding cassette homology
C:Keywords: antibiotic resistance; ATP; nucleotide binding; P-loop

F:14-200/Domain: ATP-binding cassette homology <ABC>
F:31-38/Region: nucleotide-binding motif A (P-loop)

Query Match 3.6%; Score 11; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LDEPTAGLDPL 179
Db 148 LDEPTAGLDPL 158

RESULT 13

S77760
Probable ABC-type transport protein - Mycoplasma capricolum (fragment)
N:Alternate names: protein MC453
C:Species: Mycoplasma capricolum
C:Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 16-Aug-2004
C:Accession: S77760
R:Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.; Mol. Microbiol. 16, 955-967, 1995
A:Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiology
A:Reference number: S77739; MUID:96059641; PMID:7476192
A:Accession: S77760
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-178 <SOR>
A:Cross-references: UNIPROT:Q49088; EMBL:Z33339; NID:G559469; PIDN:CAA83843.1; PID:G5604
A:Experimental source: ATCC 27343
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: ATP-binding cassette homology
C:Keywords: ATP
F:1-153/Domain: ATP-binding cassette homology (fragment) <ABCX>

Query Match 3.6%; Score 10; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 RSPFELSGGQ 150
Db 72 RSPFELSGGQ 81

RESULT 14

G83245
Probable ATP-binding component of ABC transporter PA3212 [imported] - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: G83245
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.; Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: G83245
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <STO>
A:Cross-references: UNIPROT:Q9HZ28; GB:AE004744; GB:AE004091; NID:G9949317; PIDN:AAG0660
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3212

Query Match 3.6%; Score 10; DB 2; Length 264;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LDEPTAGLDPL 178
Db 170 LDEPTAGLDPL 179

RESULT 15

AG1225
cobalt transport ATP-binding protein ChlO homolog lmo1207 [imported] - Listeria monocytogenes
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AG1225
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Anand, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.; Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1225
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-268 <GLA>
A:Cross-references: UNIPROT:Q8Y7R4; GB:NC_003210; PIDN:CAC99285.1; PID:G16410623; GSPDB:C
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1207

Query Match 3.6%; Score 10; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LDEPTAGLDPL 178
Db 161 LDEPTAGLDPL 170

Search completed: October 28, 2005, 18:16:32
Job time : 59 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 18:02:13 ; Search time 175 Seconds

(without alignments)
816.401 Million cell updates/sec

Title: US-09-769-744d-26

Perfect score: 279

Sequence: 1 MGIALENVFTYQGTPLAS.....GVSPKRLPIKIEPKESLNG 279

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	279	100.0	279	Q97N51	streptococ
2	167	59.9	279	Q8DMY0	streptococ
3	23	8.2	288	Q9CIS8	lactococcc
4	22	7.9	280	Q99X12	streptococ
5	22	7.9	280	Q7CMM8	streptococ
6	22	7.9	280	Q8DRS0	streptococ
7	22	7.9	280	Q8DWR4	streptococ
8	22	7.9	280	Q8E2L3	streptococ
9	22	7.9	280	Q8KSH2	streptococ
10	19	6.8	276	P70970	bacillus su
11	19	6.8	276	Q65P76	bacillus li
12	18	6.5	177	Q8VNL8	enterococc
13	18	6.5	288	Q8Y455	listeria mo
14	18	6.5	288	Q927N9	listeria mo
15	18	6.5	288	Q71WH8	listeria in
16	18	6.5	293	Q63H61	bacillus ce
17	18	6.5	293	Q73F66	bacillus ce
18	18	6.5	293	Q81J15	bacillus ce
19	18	6.5	293	Q81VQ1	bacillus ce
20	18	6.5	293	Q8HPM9	bacillus th
21	17	6.1	289	Q74L61	lactobacill
22	17	6.1	291	Q839D4	enterococc
23	16	5.7	295	Q88V11	lactobacill
24	16	5.7	183	Q929J2	bacillus ha
25	13	4.7	282	Q9KGD6	bacillus ha
26	12	4.3	285	Q8XWJ3	clostridium
27	12	4.3	288	Q890R3	clostridium
28	12	4.3	289	Q8ETV6	oceanobacil
29	12	4.3	297	Q51719	propionibac
30	12	4.3	304	Q98QH4	mycoplasma
31	12	4.3	305	Q6XYZ3	epioplasm

32	12	4.3	326	2	Q8TIX0	methanosarc
33	12	4.3	327	2	Q8PYH5	methanosarc
34	11	3.9	253	2	Q9YCK2	aeropyrum p
35	11	3.9	279	1	CBIO_METUA	methanococ
36	11	3.9	279	2	Q7W0L5	bordetella
37	11	3.9	279	2	Q7W230	bordetella
38	11	3.9	279	2	Q7WR08	bordetella
39	11	3.9	286	2	Q8R7Y5	thermoanaer
40	11	3.9	300	2	Q54406	streptomyce
41	11	3.9	483	2	Q8N2S4	homo sapien
42	11	3.9	546	2	Q6ABD5	propionibac
43	11	3.9	573	2	Q74DV0	geobacter s
44	11	3.9	601	2	Q8ZG45	streptomyce
45	11	3.9	856	2	Q9GMD8	homo sapien
46	11	3.9	1129	2	Q6A135	homo sapien
47	11	3.9	1623	2	Q8K449	mus musculu
48	11	3.9	1624	2	Q8IUA7	homo sapien
49	11	3.9	1624	2	Q8WUZ5	homo sapien
50	10	3.6	77	2	Q71J33	lactobacill
51	10	3.6	178	2	Q49088	mycoplasma
52	10	3.6	259	2	Q82XY5	pseudomonas
53	10	3.6	263	2	Q88RI8	pseudomonas
54	10	3.6	264	2	Q9HZ28	pseudomonas
55	10	3.6	268	2	Q8Y7R4	listeria mo
56	10	3.6	268	2	Q92CK1	listeria in
57	10	3.6	268	2	Q720M2	listeria mo
58	10	3.6	271	1	CBIO_SALTY	salmonella
59	10	3.6	271	2	Q825N5	salmonella
60	10	3.6	272	2	Q62N03	burkholderi
61	10	3.6	275	2	Q72EG7	desulfovibr
62	10	3.6	276	2	Q8TIW9	methanosarc
63	10	3.6	276	2	Q8PCS8	xanthomonas
64	10	3.6	277	2	Q50801	methanobact
65	10	3.6	277	2	Q82QH7	streptomyce
66	10	3.6	278	2	Q6AAN0	propionibac
67	10	3.6	278	2	Q9A5X8	caulobacter
68	10	3.6	279	2	Q87DX6	xylella fas
69	10	3.6	280	2	Q63XY7	burkholderi
70	10	3.6	280	2	Q8PGP5	xanthomonas
71	10	3.6	284	2	Q54187	streptomyce
72	10	3.6	285	2	Q8XNY7	clostridium
73	10	3.6	286	2	Q97EK9	clostridium
74	10	3.6	286	2	Q8CR17	staphylococ
75	10	3.6	286	2	Q9PDS7	xylella fas
76	10	3.6	288	2	Q67JX4	symbiobacte
77	10	3.6	289	2	Q8KFD6	chlorobium
78	10	3.6	292	2	Q8NNX0	corynebacte
79	10	3.6	298	2	Q8Y2M1	raistronia s
80	10	3.6	299	2	Q6AB92	propionibac
81	10	3.6	302	2	Q8EPV0	shewanella
82	10	3.6	303	1	Y180_MYCPN	mycoplasma
83	10	3.6	303	2	Q6MSQ2	mycoplasma
84	10	3.6	304	1	Y180_MYCGE	mycoplasma
85	10	3.6	308	2	Q6KHL2	streptomyce
86	10	3.6	310	2	Q829T7	mycoplasma
87	10	3.6	311	2	Q27739	streptomyce
88	10	3.6	315	2	Q6FLW4	methanobact
89	10	3.6	318	2	Q7NAQ7	mesoplasma
90	10	3.6	406	2	Q8EUF2	mycoplasma
91	10	3.6	433	2	Q9PPV2	mycoplasma
92	10	3.6	549	2	Q81Y81	ureaplasma
93	10	3.6	549	2	Q81Y81	bacillus ce
94	10	3.6	564	2	Q6HVF5	bacillus an
95	10	3.6	564	2	Q6HVF5	bacillus th
96	10	3.6	572	2	Q81AA2	bacillus ce
97	10	3.6	587	2	Q637E9	bacillus ce
98	10	3.6	587	2	Q733E4	bacillus ce
99	10	3.6	587	2	Q81Y19	bacillus an
100	10	3.6	587	2	Q6HFC3	bacillus th
101	10	3.6	601	2	Q9KDT5	bacillus ha
102	10	3.6	610	2	Q8ERA0	oceanobacil
103	10	3.6	888	2	Q7RBT4	plasmocodium
104	10	3.6	888	2	Q7RBT4	plasmocodium

105	10	3.6	1543	2	Q8WVZ4	Q8wvz4 homo sapien	178	9	3.2	500	2	Q8U7X8	Q8u7x8 agrobacteri
106	10	3.6	1543	2	Q7Z2I9	Q7z2i9 homo sapien	179	9	3.2	503	2	Q8AB11	Q8ab11 bacteroides
107	10	3.6	1574	2	Q69ZY4	Q69zy4 mus musculus	180	9	3.2	505	2	Q9CL10	Q9cl10 pasteurella
108	10	3.6	1591	2	Q94911	Q94911 homo sapien	181	9	3.2	508	2	Q92XH3	Q92xh3 rhizobium m
109	10	3.6	1620	2	Q8K440	Q8k440 mus musculus	182	9	3.2	528	2	Q82BT2	Q82bt2 streptomyce
110	10	3.6	1620	2	Q8K442	Q8k442 mus musculus	183	9	3.2	545	2	Q637L3	Q637l3 bacillus ce
111	9	3.2	126	2	Q84JX9	Q84jx9 arabidopsis	184	9	3.2	554	2	Q67511	Q67511 aquifex aeo
112	9	3.2	126	2	Q84VL1	Q84vl1 arabidopsis	185	9	3.2	559	2	Q7W090	Q7w090 bordetella
113	9	3.2	168	2	Q899Y3	Q899y3 clostridium	186	9	3.2	559	2	Q7W3L1	Q7w3l1 bordetella
114	9	3.2	194	2	Q8DM53	Q8dm53 synecococc	187	9	3.2	565	2	Q9CIN1	Q9cin1 lactococcus
115	9	3.2	201	1	CCMA_RHILO	Q98ea4 rhizobium l	188	9	3.2	566	2	Q7WEY6	Q7wey6 bordetella
116	9	3.2	209	2	Q7VBR6	Q7vbr6 prochloroco	189	9	3.2	579	2	Q7P0D7	Q7p0d7 chromobacte
117	9	3.2	210	2	Q55649	Q55649 synecocyst	190	9	3.2	580	1	MDLB_BUCAI	P57552 buchnera ap
118	9	3.2	210	2	Q7V7F8	Q7v7f8 prochloroco	191	9	3.2	580	1	Q7MJW4	Q7mjw4 vibrio vuln
119	9	3.2	214	2	Q7U732	Q7u732 synecococc	192	9	3.2	591	2	Q8DAA9	Q8daa9 vibrio vuln
120	9	3.2	215	2	Q7V225	Q7v225 prochloroco	193	9	3.2	591	2	Q6D816	Q6d816 erwiniia car
121	9	3.2	215	2	Q8DJC9	Q8djcc synecococc	194	9	3.2	592	2	Q6LTJ3	Q6ltj3 photobacter
122	9	3.2	224	2	Q8YMQ7	Q8ymq7 anabaena sp	195	9	3.2	592	2	Q87PS0	Q87ps0 vibrio para
123	9	3.2	242	2	Q9HPH7	Q9hph7 halobacteri	196	9	3.2	593	1	MDLB_ECOLI	P75706 escherichia
124	9	3.2	244	2	Q8KFK0	Q8kfk0 chlorobium	197	9	3.2	593	2	Q8Z8U4	Q8z8u4 salmonella
125	9	3.2	246	2	Q67R20	Q67r20 symbiobacte	198	9	3.2	593	2	Q8ZRB3	Q8zrb3 salmonella
126	9	3.2	247	2	Q7V4Q8	Q7v4q8 prochloroco	199	9	3.2	594	2	Q7UD14	Q7udi4 shigella fl
127	9	3.2	248	2	Q6MHX2	Q6mhx2 bdellovibri	200	9	3.2	594	2	Q7N0M4	Q7n0m4 photorhabdu
128	9	3.2	248	2	Q822Q2	Q822q2 chlamydophi	201	9	3.2	605	2	P72607	P72607 synecocyst
129	9	3.2	251	2	Q7U9P2	Q7u9p2 synecococc	202	9	3.2	607	2	Q66DS1	Q66ds1 yersinia ps
130	9	3.2	256	2	Q74HR9	Q74hr9 lactobacilli	203	9	3.2	607	2	Q8ZC78	Q8zc78 yersinia pe
131	9	3.2	260	2	P72734	P72734 synecocyst	204	9	3.2	611	2	Q9CIU5	Q9cius lactococcus
132	9	3.2	260	2	P73030	P73030 synecocyst	205	9	3.2	616	2	Q8D152	Q8d152 yersinia pe
133	9	3.2	260	2	Q820B8	Q8z0b8 anabaena sp	206	9	3.2	631	2	Q83M47	Q83m47 shigella fl
134	9	3.2	262	2	Q7NDM8	Q7ndm8 gloebacter	207	9	3.2	646	2	Q6MCG4	Q6mcg4 parachlamyd
135	9	3.2	267	2	Q7UXL9	Q7uxl9 rhodopirell	208	9	3.2	697	1	YN26_MYCTU	P63399 mycobacteri
136	9	3.2	268	2	Q8DLZ8	Q8dlz8 synecococc	209	9	3.2	697	1	YN53_MYCBO	P63400 mycobacteri
137	9	3.2	270	2	Q7VDP7	Q7vdp7 prochloroco	210	9	3.2	714	2	Q73Y59	Q73y59 mycobacteri
138	9	3.2	271	2	Q7P788	Q7p788 fusbacteri	211	9	3.2	724	2	Q9CCF9	Q9ccf9 mycobacteri
139	9	3.2	271	2	Q8RHK9	Q8rhk9 fusbacteri	212	9	3.2	726	2	Q32971	Q32971 mycobacteri
140	9	3.2	272	2	Q7V306	Q7v306 prochloroco	213	9	3.2	749	2	Q8KJR6	Q8kjr6 gordonia ap
141	9	3.2	278	2	Q9Z9J3	Q9z9j3 bacillus ha	214	9	3.2	945	2	Q9N8D9	Q9n8d9 trypanosoma
142	9	3.2	279	2	Q6ASX4	Q6asx4 oryza sativ	215	9	3.2	948	2	Q85ZU4	Q85zu4 borrelia ga
143	9	3.2	279	2	Q748K0	Q748k0 geobacter s	216	9	3.2	950	2	Q51770	Q51770 borrelia bu
144	9	3.2	280	2	Q68106	Q68106 rhodobacter	217	9	3.2	960	2	Q73V82	Q73v82 mycobacteri
145	9	3.2	281	2	Q7Y189	Q7y189 oryza sativ	218	9	3.2	1031	2	Q7URK7	Q7urk7 rhodopirell
146	9	3.2	282	2	Q74L62	Q74l62 lactobacilli	219	9	3.2	1175	2	Q8XNW6	Q8xnw6 clostridium
147	9	3.2	285	2	Q29256	Q29256 archaeoglob	220	9	3.2	1222	2	Q8KDA7	Q8kda7 chlorobium
148	9	3.2	286	2	Q99548	Q99548 staphylococ	221	9	3.2	1465	2	Q70WG4	Q70wg4 barley yell
149	9	3.2	286	2	Q7A088	Q7a088 staphylococ	222	9	3.2	2258	1	POL1_BAMMN	P90245 b genome po
150	9	3.2	286	2	Q7A471	Q7a471 staphylococ	223	9	3.2	2258	2	Q55459	Q55459 barley mild
151	9	3.2	286	2	Q6G7A0	Q6g7a0 staphylococ	224	9	3.2	2258	2	Q93128	Q93128 barley mild
152	9	3.2	286	2	Q6GEL4	Q6gel4 staphylococ	225	9	3.2	2258	2	Q65654	Q65654 barley mild
153	9	3.2	288	2	Q9KFP34	Q9kf34 bacillus ha	226	9	3.2	2258	2	Q68VH7	Q68vh7 barley mild
154	9	3.2	289	2	Q7NNH5	Q7nnh5 gloebacter	227	9	3.2	2258	2	Q68VH8	Q68vh8 barley mild
155	9	3.2	290	2	Q634W2	Q634w2 bacillus ce	228	9	3.2	2258	2	Q68VH9	Q68vh9 barley mild
156	9	3.2	290	2	Q730W8	Q730w8 bacillus ce	229	9	3.2	2258	2	Q9WAA3	Q9waa3 barley mild
157	9	3.2	290	2	Q818M8	Q818m8 bacillus ce	230	9	3.2	2261	2	Q71BF1	Q71bf1 barley mild
158	9	3.2	290	2	Q81M11	Q81m11 bacillus an	231	9	3.2	2404	2	Q9QBG1	Q9qbg1 wheat yello
159	9	3.2	290	2	Q6HDU2	Q6hdu2 bacillus th	232	9	3.2	2404	2	Q9QBG4	Q9qbg4 wheat yello
160	9	3.2	292	2	Q8EG59	Q8eg59 shewanella	233	9	3.2	2407	2	Q9QMA1	Q9qma1 wheat yello
161	9	3.2	293	2	Q8YTP2	Q8ytp2 anabaena sp	234	9	3.2	2410	1	POL1_BAYMJ	Q01206 b genome po
162	9	3.2	294	2	Q9A2J5	Q9a2j5 caulobacter	235	9	3.2	2410	2	Q9YJW3	Q9yjlw3 barley yell
163	9	3.2	295	2	Q8GF30	Q8gf30 zymomonas m	236	9	3.2	2411	2	Q71BD5	Q71bd5 barley yell
164	9	3.2	296	2	Q897T0	Q897t0 clostridium	237	9	3.2	2412	1	POL1_BAYNG	Q04574 b genome po
165	9	3.2	297	2	Q8PMN7	Q8pmn7 xanthomonas	238	9	3.2	2412	2	Q70WS1	Q70ws1 barley yell
166	9	3.2	301	2	Q8CU34	Q8cu34 staphylococ	239	9	3.2	2412	2	Q70WS2	Q70ws2 barley yell
167	9	3.2	302	2	Q8NLB0	Q8nlb0 corynebacte	240	9	3.2	2412	2	Q70WS3	Q70ws3 barley yell
168	9	3.2	303	2	Q6NH47	Q6nh47 corynebacte	241	9	3.2	2412	2	Q70WS4	Q70ws4 barley yell
169	9	3.2	305	2	Q6M1H8	Q6m1h8 corynebacte	242	9	3.2	2412	2	Q70WS5	Q70ws5 barley yell
170	9	3.2	306	2	Q643B2	Q643b2 streptomyce	243	9	3.2	2412	2	Q70WS6	Q70ws6 barley yell
171	9	3.2	330	2	Q83H10	Q83h10 tropheryma	244	9	3.2	2412	2	Q70WS7	Q70ws7 barley yell
172	9	3.2	345	2	Q9AT00	Q9at00 arabidopsis	245	8	2.9	49	2	Q8XL26	Q8xl26 clostridium
173	9	3.2	346	2	Q83GR9	Q83gr9 tropheryma	246	8	2.9	108	2	Q9F6K2	Q9f6k2 brucella ab
174	9	3.2	364	2	Q80812	Q80812 arabidopsis	247	8	2.9	116	2	Q9QUT1	Q9qut1 mus musculus
175	9	3.2	472	2	Q7CUM3	Q7cum3 agrobacteri	248	8	2.9	208	1	URK_CLOPE	Q8xji6 clostridium
176	9	3.2	496	2	Q669F1	Q669f1 yersinia ps	249	8	2.9	212	2	Q892J8	Q892j8 clostridium
177	9	3.2	496	2	Q82DQ6	Q82dq6 yersinia pe	250	8	2.9	213	2	Q88UY6	Q88uy6 lactobacilli

251	8	2.9	215	1	CCWA_BRUMS	Q8vems brucella me	324	8	2.9	307	2	Q6NFA4	Q6nfa4 corynebacte
252	8	2.9	215	1	CCWA_BRUSU	Q8g358 brucella su	325	8	2.9	308	2	Q62GD4	Q62gd4 burkholderi
253	8	2.9	215	1	I12A_MOUSE	P43431 mus musculu	326	8	2.9	308	2	Q91008	Q91008 streptomyce
254	8	2.9	216	2	Q9KIR3	Q9kir3 neisseria m	327	8	2.9	311	2	Q9A3C4	Q9a3c4 caulobacter
255	8	2.9	222	2	Q7VI23	Q7vi23 helicobacte	328	8	2.9	313	2	Q63Q81	Q63q81 burkholderi
256	8	2.9	224	2	Q7N0N3	Q7n0n3 photorhabdu	329	8	2.9	319	2	Q9HK71	Q9hk71 thermoplasma
257	8	2.9	226	2	Q8XN98	Q8xn98 clostridium	330	8	2.9	321	2	Q974E9	Q974e9 sulfobolus
258	8	2.9	229	2	Q10689	Q10689 cymbidium m	331	8	2.9	321	2	Q8XV75	Q8xv75 ralstonia s
259	8	2.9	229	2	Q6PY93	Q6py93 cymbidium m	332	8	2.9	334	2	Q6ARS3	Q6ars3 desulfotale
260	8	2.9	229	2	Q705K6	Q705k6 cymbidium m	333	8	2.9	334	2	Q8VQL8	Q8vql8 brucella ab
261	8	2.9	230	2	Q7VHG6	Q7vhg6 helicobacte	334	8	2.9	358	2	Q8PD85	Q8pd85 xanthomonas
262	8	2.9	231	2	Q7VHG6	Q7vhg6 helicobacte	335	8	2.9	377	2	Q8YDI3	Q8ydi3 brucella me
263	8	2.9	231	2	Q8UCS3	Q8ucs3 agrobacteri	336	8	2.9	382	2	Q99ZS8	Q99zs8 streptococc
264	8	2.9	233	2	Q37154	Q37154 cymbidium m	337	8	2.9	384	2	Q7CN92	Q7cn92 streptococc
265	8	2.9	233	2	Q9Q3U7	Q9q3u7 cymbidium m	338	8	2.9	384	2	Q8DUF7	Q8duf7 streptococc
266	8	2.9	234	2	Q74DN5	Q74dn5 geobacter s	339	8	2.9	384	2	Q8DZJ0	Q8dzj0 streptococc
267	8	2.9	237	2	Q30194	Q30194 archaeoglob	340	8	2.9	384	2	Q8E554	Q8e554 streptococc
268	8	2.9	238	2	Q97MF3	Q97mf3 clostridium	341	8	2.9	384	2	Q8K7K4	Q8k7k4 streptococc
269	8	2.9	239	2	Q8CUI3	Q8cuy3 oceanobacil	342	8	2.9	385	2	Q97Q42	Q97q42 streptococc
270	8	2.9	243	2	Q8NR42	Q8nr42 corynebacte	343	8	2.9	385	2	Q8DPC2	Q8dpc2 streptococc
271	8	2.9	243	2	Q8PT24	Q8pt24 bradyrhizob	344	8	2.9	390	2	Q8ZS21	Q8zs21 anabaena sp
272	8	2.9	244	2	Q7NNW9	Q7nnw9 geobacter	345	8	2.9	406	2	Q89B71	Q89b71 bradyrhizob
273	8	2.9	246	2	Q612U3	Q612u3 bacillus an	346	8	2.9	407	2	Q9YOH0	Q9yoh0 tetrahymena
274	8	2.9	248	2	Q29435	Q29435 archaeoglob	347	8	2.9	416	2	Q9YOH5	Q9yoh5 tetrahymena
275	8	2.9	248	2	Q8UAL3	Q8ual3 agrobacteri	348	8	2.9	420	2	Q9YF81	Q9yfe1 aeropyrum p
276	8	2.9	249	2	Q9AX28	Q9ax28 oryza sativ	349	8	2.9	428	2	Q9CGD4	Q9cgd4 lactococcus
277	8	2.9	249	2	Q06529	Q06529 lactobacill	350	8	2.9	448	2	Q6FQ90	Q6fq90 candida gla
278	8	2.9	249	2	Q9FCU6	Q9fcu6 lactobacill	351	8	2.9	474	2	Q8PQ56	Q8pq56 xanthomonas
279	8	2.9	249	2	Q74DN5	Q74dn5 geobacter s	352	8	2.9	484	2	Q7VF91	Q7vf91 helicobacte
280	8	2.9	250	1	PS7B_PYRAE	Q8zx91 pyrobaculum	353	8	2.9	499	2	Q7CEQ8	Q7ceq8 streptococc
281	8	2.9	250	2	Q8VUH2	Q8vuh2 streptococc	354	8	2.9	506	2	Q9PPT0	Q9ppt0 methanosarc
282	8	2.9	250	2	Q731L0	Q731l0 treponema d	355	8	2.9	507	2	Q6LUY1	Q6luy1 photobacter
283	8	2.9	250	2	Q8DUD2	Q8dud2 streptococc	356	8	2.9	507	2	Q6LUY1	Q6luy1 photobacter
284	8	2.9	250	2	Q8DZX1	Q8dxx1 streptococc	357	8	2.9	507	2	Q8UAZ4	Q8uaz4 agrobacteri
285	8	2.9	250	2	Q8E5M1	Q8e5m1 streptococc	358	8	2.9	510	2	Q663Y5	Q663y5 yersinia ps
286	8	2.9	250	2	Q8UCH3	Q8uch3 agrobacteri	359	8	2.9	510	2	Q6DB03	Q6db03 yersinia pe
287	8	2.9	251	2	Q8TS12	Q8ts12 methanosarc	360	8	2.9	513	2	Q6DB03	Q6db03 erwinia car
288	8	2.9	252	2	Q97085	Q97085 clostridium	361	8	2.9	514	2	Q894X5	Q894x5 clostridium
289	8	2.9	255	2	Q6ABL6	Q6abl6 propionibac	362	8	2.9	518	2	Q8L241	Q8l241 salmonella
290	8	2.9	255	2	Q7MBY2	Q7mby2 wolfinella s	363	8	2.9	523	2	Q7WTH8	Q7wth8 escherichia
291	8	2.9	256	2	Q62H61	Q62h61 burkholderi	364	8	2.9	527	2	Q8YOM7	Q8yom7 ralstonia s
292	8	2.9	256	2	Q63R21	Q63r21 burkholderi	365	8	2.9	527	2	Q7P2D6	Q7p2d6 fusobacteri
293	8	2.9	257	2	Q8VVF9	Q8vvf9 streptococc	366	8	2.9	527	2	Q8RHU5	Q8rhu5 fusobacteri
294	8	2.9	257	2	Q8VVG3	Q8vvg3 streptococc	367	8	2.9	540	2	Q9KPI2	Q9kpi2 vibrio chol
295	8	2.9	258	2	Q9K468	Q9k468 streptomyce	368	8	2.9	541	2	Q81HE3	Q81he3 bacillus ce
296	8	2.9	258	2	Q6AIP0	Q6aip0 desulfotale	369	8	2.9	543	2	Q8NXQ3	Q8nxq3 staphylococ
297	8	2.9	259	2	Q97E47	Q97e47 clostridium	370	8	2.9	543	2	Q932E9	Q932e9 staphylococ
298	8	2.9	259	2	Q9CBT4	Q9cet4 lactococcus	371	8	2.9	543	2	Q99VT7	Q99vt7 staphylococ
299	8	2.9	260	2	Q6A7M6	Q6a7m6 propionibac	372	8	2.9	543	2	Q6GBE6	Q6gbe6 staphylococ
300	8	2.9	262	2	Q73NH4	Q73nh4 treponema d	373	8	2.9	549	2	Q6GIV8	Q6giv8 staphylococ
301	8	2.9	263	2	Q880B4	Q880b4 pseudomonas	374	8	2.9	549	2	Q62J78	Q62j78 burkholderi
302	8	2.9	263	2	Q9RKT3	Q9rkt3 streptomyce	375	8	2.9	549	2	Q63SX1	Q63sx1 burkholderi
303	8	2.9	265	2	Q9S1F1	Q9s1f1 vibrio chol	376	8	2.9	549	2	Q98K72	Q98k72 rhizobium l
304	8	2.9	269	2	Q89H05	Q89h05 bradyrhizob	377	8	2.9	549	2	Q7WNN2	Q7wnn2 bordetella
305	8	2.9	274	2	Q8V5U5	Q8v5u5 listeria mo	378	8	2.9	550	2	Q6ANY7	Q6any7 desulfotale
306	8	2.9	274	2	Q92A48	Q92a48 listeria mo	379	8	2.9	551	2	Q6A6S5	Q6a6s5 propionibac
307	8	2.9	274	2	Q71Y54	Q71y54 listeria mo	380	8	2.9	552	2	Q6LPY6	Q6lpy6 photobacter
308	8	2.9	275	2	Q7CS95	Q7cs95 agrobacteri	381	8	2.9	554	2	Q7QN86	Q7qn86 anopheles g
309	8	2.9	278	2	Q6LX68	Q6lx68 methanococc	382	8	2.9	555	2	Q6ACM0	Q6acm0 leifsonia x
310	8	2.9	280	2	Q882J7	Q882j7 pseudomonas	383	8	2.9	556	2	Q89P20	Q89p20 bradyrhizob
311	8	2.9	280	2	Q82LM9	Q82lm9 streptomyce	384	8	2.9	557	2	Q9K5W6	Q9k5w6 bacillus ha
312	8	2.9	281	2	Q8XHV2	Q8xhv2 clostridium	385	8	2.9	560	2	Q74IR3	Q74ir3 lactobacill
313	8	2.9	283	2	Q7W2Y9	Q7w2y9 bordetella	386	8	2.9	564	2	Q8CTJ5	Q8ctj5 staphylococ
314	8	2.9	283	2	Q7WDY9	Q7wdy9 bordetella	387	8	2.9	568	2	Q73HY8	Q73hy8 wolbachia p
315	8	2.9	283	2	Q83DG0	Q83dg0 coxiella bu	388	8	2.9	569	2	Q88H94	Q88h94 pseudomonas
316	8	2.9	287	2	Q67JX3	Q67jx3 symbiobacte	389	8	2.9	571	2	Q54121	Q54121 staphylococ
317	8	2.9	289	2	Q9F1W2	Q9f1w2 streptomyce	390	8	2.9	578	2	Q73X96	Q73x96 mycobacteri
318	8	2.9	289	2	Q6FFK1	Q6ffk1 acinetobact	391	8	2.9	581	2	Q8UOD8	Q8uod8 pyrococcus
319	8	2.9	291	2	Q8PA14	Q8pa14 xanthomonas	392	8	2.9	581	2	Q74HD4	Q74hd4 lactobacill
320	8	2.9	291	2	Q8PM85	Q8pm85 xanthomonas	393	8	2.9	581	2	Q8PF61	Q8pf61 corynebacte
321	8	2.9	298	2	Q9REN4	Q9ren4 zymomonas m	394	8	2.9	583	1	EXP8_STRPN	P35538 streptococc
322	8	2.9	298	2	Q892V1	Q892v1 clostridium	395	8	2.9	583	2	Q9URY4	Q9ury4 schizosacch
323	8	2.9	300	2	Q7P0X8	Q7p0x8 chromobacte	396	8	2.9	583	2	Q8DNL4	Q8dnl4 streptococc

397	8	2.9	588	2	Q7NCV8	Q7ncv8 gloeobacter	470	7	2.5	88	1	RS15_PHOLU	P41120 photorhabdu
398	8	2.9	589	2	Q8RGT4	Q8rgt4 fusobacteri	471	7	2.5	89	2	Q9NQ1	Q9nq1 leishmania
399	8	2.9	589	2	Q8EV13	Q8ev13 mycoplasma	472	7	2.5	89	2	Q9AMN7	Q9awn7 oryza sativ
400	8	2.9	590	2	Q8PVR0	Q8per0 methanosarc	473	7	2.5	89	2	Q7MY9	Q7my9 photorhabdu
401	8	2.9	590	2	Q7V0Z5	Q7v0z5 prochlorococ	474	7	2.5	94	2	Q8DT21	Q8dt21 streptococc
402	8	2.9	594	2	Q834D4	Q834d4 enterococcu	475	7	2.5	95	1	Y736_ARCFU	Q29522 archaeoglob
403	8	2.9	595	2	Q30410	Q30410 bacillus br	476	7	2.5	109	2	Q9B034	Q9b034 bacterioph
404	8	2.9	595	2	Q82WGO	Q82wgo nitrosomona	477	7	2.5	111	2	Q9DB78	Q9db78 mus musculu
405	8	2.9	596	1	ABCL_ENCCU	Q8eq15 encephalito	478	7	2.5	119	2	Q30353	Q30353 cervus elap
406	8	2.9	600	2	Q8SQV1	Q8sqv1 encephalito	479	7	2.5	123	2	Q67MY3	Q67my3 symbiobacte
407	8	2.9	600	2	Q93GX8	Q93gx8 streptomyc	480	7	2.5	126	2	Q6LNU3	Q6lnz3 photobacter
408	8	2.9	600	2	Q7NBB3	Q7nbb3 mycoplasma	481	7	2.5	127	2	Q96MJ2	Q96mj2 homo sapien
409	8	2.9	601	2	Q8Y6N3	Q8y6n3 listeria mo	482	7	2.5	132	2	Q65X68	Q65x68 oryza sativ
410	8	2.9	601	2	Q82B59	Q82b59 listeria in	483	7	2.5	134	2	Q982A2	Q982a2 streptomyc
411	8	2.9	601	2	Q7I219	Q7i219 listeria mo	484	7	2.5	137	2	Q67RT2	Q67rt2 symbiobacte
412	8	2.9	603	2	Q7MJF9	Q7mjf9 vibrio vuln	485	7	2.5	142	2	Q8W60	Q8w60 homo sapien
413	8	2.9	604	2	Q6AAAF8	Q6aaf8 propionibac	486	7	2.5	143	1	COTP_BACSU	P96698 bacillus su
414	8	2.9	606	2	Q44940	Q44940 drosophila	487	7	2.5	147	2	Q9KK03	Q9kk03 pseudomonas
415	8	2.9	606	2	Q8SX41	Q8sx41 drosophila	488	7	2.5	148	2	Q7NOM8	Q7nom8 photorhabdu
416	8	2.9	606	2	Q7KWB2	Q7kwb2 drosophila	489	7	2.5	150	2	Q8DP35	Q8dp35 streptococc
417	8	2.9	606	2	Q8YMH8	Q8ymh8 anabaena sp	490	7	2.5	151	2	Q9ANS4	Q9ans4 rhodobacter
418	8	2.9	607	2	Q6Y8R0	Q6y8r0 mycoplasma	491	7	2.5	153	2	Q6M0J2	Q6m0j2 methanococc
419	8	2.9	608	2	Q73JW5	Q73jw5 treponema d	492	7	2.5	154	2	Q6G1F3	Q6g1f3 bartonella
420	8	2.9	608	2	Q9CG38	Q9cg38 lactococcus	493	7	2.5	155	2	Q7QRK5	Q7qrk5 giardia lam
421	8	2.9	614	2	Q8TQ05	Q8tq05 methanosarc	494	7	2.5	157	2	Q860L5	Q860l5 syncerus ca
422	8	2.9	614	2	Q8F141	Q8f141 mesoplasma	495	7	2.5	158	2	Q8L490	Q8l490 oryza sativ
423	8	2.9	626	2	Q7NIB9	Q7nib9 gloeobacter	496	7	2.5	158	2	Q67JD2	Q67jd2 symbiobacte
424	8	2.9	636	2	Q9S368	Q9s368 neisseria g	497	7	2.5	162	2	Q19804	Q19804 caenorhabdi
425	8	2.9	636	2	Q9XAZ9	Q9xaz9 neisseria g	498	7	2.5	162	2	Q82RA8	Q82ra8 streptomyc
426	8	2.9	636	2	Q9JZH4	Q9jzh4 neisseria m	499	7	2.5	167	2	Q9AKT6	Q9akt6 paenibacill
427	8	2.9	646	2	Q84265	Q84266 chlamydia t	500	7	2.5	168	2	Q6CUI3	Q6cui3 kluyveromyc
428	8	2.9	646	2	Q8WC12	Q8wc12 parachlamyd	501	7	2.5	170	2	Q6PYC4	Q6pyc4 rhizobium m
429	8	2.9	647	2	Q9PKD0	Q9pkd0 chlamydia m	502	7	2.5	171	2	Q7ZST0	Q7zst0 human immun
430	8	2.9	650	2	Q8Y5I9	Q8y5i9 listeria mo	503	7	2.5	172	2	Q6D354	Q6d354 erwinia car
431	8	2.9	650	2	Q929U5	Q929u5 listeria in	504	7	2.5	174	2	Q8YL81	Q8yl81 anabaena sp
432	8	2.9	650	2	Q71XU0	Q71xu0 listeria mo	505	7	2.5	174	2	Q97RH8	Q97rh8 streptococc
433	8	2.9	666	2	Q63FP6	Q63ff6 bacillus ce	506	7	2.5	175	2	Q8BPZ5	Q8bpz5 mus musculu
434	8	2.9	666	2	Q73CX1	Q73cx1 bacillus ce	507	7	2.5	176	2	Q74LJ8	Q74lj8 mycobacteri
435	8	2.9	666	2	Q6HMH8	Q6hmh8 bacillus th	508	7	2.5	176	2	Q7MGV9	Q7mgv9 vibrio vuln
436	8	2.9	672	2	Q65LV8	Q65lv8 bacillus li	509	7	2.5	176	2	Q8DCY7	Q8dcy7 vibrio vuln
437	8	2.9	673	2	Q07549	Q07549 bacillus su	510	7	2.5	178	2	Q6AGS6	Q6ag56 leifsonia x
438	8	2.9	674	2	Q9KDD3	Q9kdd3 bacillus ha	511	7	2.5	180	2	Q6CZF6	Q6czf6 erwinia car
439	8	2.9	676	2	Q8CUK8	Q8cuk8 oceanobacil	512	7	2.5	181	2	P71891	P71891 mycobacteri
440	8	2.9	677	2	Q9HOG8	Q9hog8 arabidopsis	513	7	2.5	181	2	Q7TYT9	Q7tyt9 mycobacteri
441	8	2.9	678	2	Q9FUT3	Q9fut3 arabidopsis	514	7	2.5	183	2	Q8UBK1	Q8ubk1 agrobacteri
442	8	2.9	680	2	Q9M0G9	Q9m0g9 arabidopsis	515	7	2.5	185	2	Q8PD12	Q8pd12 xanthomonas
443	8	2.9	690	1	ATM1_YEAST	P40416 saccharomyc	516	7	2.5	185	2	Q6FUA4	Q6fua4 candida gla
444	8	2.9	691	2	Q751N2	Q751n2 ashbya gos	517	7	2.5	187	2	Y176_SULTO	Q97615 sulfolobus
445	8	2.9	696	2	Q6BXD7	Q6bxd7 debaryomyc	518	7	2.5	188	1	RUVA_WOLSU	Q7ma70 wolfinella s
446	8	2.9	710	2	Q6C6N0	Q6c6n0 yarrowia li	519	7	2.5	189	1	Q704N6	Q704n6 sugarcane y
447	8	2.9	720	2	Q6CX96	Q6cx96 kluyveromyc	520	7	2.5	189	2	Q704N6	Q704n6 sulfolobus
448	8	2.9	722	2	Q9F445	Q9f445 streptococc	521	7	2.5	190	2	Q970B3	Q970b3 chlorobium
449	8	2.9	727	2	Q6FMS9	Q6fms9 candida gla	522	7	2.5	191	2	Q8KCL0	Q8kcl0 bacillus su
450	8	2.9	728	2	Q9LPF78	Q9lpf78 arabidopsis	523	7	2.5	197	1	CYC1_BACSU	Q34577 bacillus li
451	8	2.9	728	2	Q9LVM1	Q9lvm1 arabidopsis	524	7	2.5	197	2	Q65JT8	Q65jt8 bacillus li
452	8	2.9	733	2	Q658I3	Q658i3 oryza sativ	525	7	2.5	200	2	Q7P7R5	Q7p7r5 fusobacteri
453	8	2.9	738	2	Q6D228	Q6d228 erwinia car	526	7	2.5	200	2	Q8UJF5	Q8ujf5 agrobacteri
454	8	2.9	756	2	Q8BX70	Q8bx70 lactobacill	527	7	2.5	201	1	COAB_CLOAB	Q97k22 clostridium
455	8	2.9	767	2	Q8NZE2	Q8nze2 streptococc	528	7	2.5	201	2	Q8AAQ1	Q8aaq1 bacteroides
456	8	2.9	781	2	Q7QWE0	Q7qwe0 giardia lam	529	7	2.5	202	2	Q64VR1	Q64vr1 bacteroides
457	8	2.9	788	2	Q73FZ8	Q73fz8 wolbachia p	530	7	2.5	204	1	KGUA_BACTN	Q8a677 bacteroides
458	8	2.9	810	2	Q8G838	Q8g838 bifidobacte	531	7	2.5	204	2	Q64PY1	Q64py1 bacteroides
459	8	2.9	820	2	Q9KEY5	Q9key5 bacillus ha	532	7	2.5	205	2	Q99ZT5	Q99zt5 streptococc
460	8	2.9	1062	2	Q6VTH1	Q6vth1 chlamydomon	533	7	2.5	206	1	COAB_PASMU	Q9cpf5 pasteurella
461	8	2.9	1167	1	CARB_RHILO	Q8rcy8 rhizobium l	534	7	2.5	206	1	CYSC_BUCAI	P57497 buchnera ap
462	8	2.9	1177	2	Q8RCY8	Q8rcy8 thermosanaer	535	7	2.5	206	2	Q8YQ85	Q8yq85 anabaena sp
463	8	2.9	1293	2	Q9V748	Q9v748 emericella	536	7	2.5	206	2	Q9QSB4	Q9qsb4 human immun
464	8	2.9	1318	2	Q9VJ21	Q9vj21 drosophila	537	7	2.5	207	1	CYSC_LACPL	Q88x60 lactobacill
465	8	2.9	1323	1	HS16_CANAL	P53706 candida alb	538	7	2.5	207	2	Q9PAT3	Q9fat3 vibrio para
466	8	2.9	1637	2	Q9VRG5	Q9vrg5 drosophila	539	7	2.5	208	1	COAB_WIGER	Q8d308 wiggleswort
467	7	2.5	52	2	Q6KEB8	Q6keb8 homo sapien	540	7	2.5	208	1	CYC2_BACHD	Q9k7h6 bacillus ha
468	7	2.5	52	2	Q71V93	Q71v93 ovis aries	541	7	2.5	209	1	LOLB_HAEIN	P45270 haemophilus
469	7	2.5	68	2	Q69619	Q69619 human immun	542	7	2.5	209	1	URK_CLOTE	Q896e3 clostridium

543	7	2.5	212	2	Q7U576	Q7U576 synechococ	616	7	2.5	238	1	ZNUC_BUCBP	Q89aj0 buchnera ap
544	7	2.5	212	2	Q9UJQ4	Q9Jjq4 mus musculu	617	7	2.5	239	2	Q860K6	Q860k6 tragalaphus
545	7	2.5	214	2	Q65VP4	Q65vp4 mannhemita	618	7	2.5	240	1	Y124_THEMA	Q9wx8 thermotoga
546	7	2.5	215	2	Q9JJQ7	Q9jjq7 mus musculu	619	7	2.5	240	2	O18131	O18131 caenorhabdi
547	7	2.5	215	2	Q9JJQ8	Q9jjq8 mus musculu	620	7	2.5	240	2	Q2DL2	Q2dl2 listeria in
548	7	2.5	216	2	Q65Y02	Q65y02 bombyx mori	621	7	2.5	240	2	Q8N749	Q8n749 rhodopseudo
549	7	2.5	216	2	Q8EMH7	Q8emh7 mycoplasma	622	7	2.5	240	2	Q6D1A9	Q6dia9 erwinia car
550	7	2.5	217	2	Q8SSJ6	Q8ssj6 encephalico	623	7	2.5	244	2	Q6UP75	Q6up75 alcaligenes
551	7	2.5	218	1	KCV_FUSNN	Q8saj6 fusobacteri	624	7	2.5	244	2	Q8RIR9	Q8rir9 fusobacteri
552	7	2.5	218	2	Q8TZW8	Q8tri8 fusobacteri	625	7	2.5	244	2	Q87JTS	Q87jt5 vibrio para
553	7	2.5	219	2	Q8ZXP8	Q8tzw8 pyrococcus	626	7	2.5	245	2	Q7DM58	Q7dm58 arabidopsis
554	7	2.5	219	2	Q750E1	Q8zxp8 pyrobaculum	627	7	2.5	245	2	Q8M391	Q8m391 corynebacte
555	7	2.5	219	2	Q7P7N3	Q750e1 ashbya goss	628	7	2.5	245	2	Q81X89	Q8lx89 bacillus an
556	7	2.5	220	2	Q9Z6L8	Q7p7n3 fusobacteri	629	7	2.5	246	1	NATA_BACSU	P46903 bacillus su
557	7	2.5	222	2	Q87TW3	Q9z6l8 listeria in	630	7	2.5	246	2	Q6MLX6	Q6mlx6 bdellovibri
558	7	2.5	222	2	Q8FTL1	Q87tw3 pseudomonas	631	7	2.5	247	2	Q8ZVX1	Q8zvx1 pyrobaculum
559	7	2.5	223	1	GIDB_CORGL	Q8ftl1 corynebacte	632	7	2.5	247	2	Q81EP0	Q8lep0 bacillus ce
560	7	2.5	223	2	Q7X057	Q8nl53 corynebacte	633	7	2.5	248	2	Q6FILL	Q6fll1 mesoplasma
561	7	2.5	223	2	Q6VQY4	Q7x057 uncultured	634	7	2.5	248	2	Q829V5	Q829v5 streptomyce
562	7	2.5	224	2	Q8RDY9	Q6vqy4 onion yello	635	7	2.5	249	2	Q8GEX2	Q8gev2 methylobact
563	7	2.5	224	2	Q8RDY9	Q8rdy9 fusobacteri	636	7	2.5	249	2	Q8NN48	Q8nn48 corynebacte
564	7	2.5	225	2	Q65TW5	Q65tw5 mannhemita	637	7	2.5	249	2	O8UJE3	O8uje3 agrobacteri
565	7	2.5	225	2	Q8W82	Q8w82 lactobacill	638	7	2.5	249	2	Q6N2L3	Q6n2l3 rhodopseudo
566	7	2.5	226	2	Q8GP10	Q8w82 staphylococ	639	7	2.5	250	2	Q748L6	Q748l6 geobacter s
567	7	2.5	227	1	CORE_CLOTE	Q8gp10 staphylococ	640	7	2.5	250	2	Q7MAP5	Q7map5 wolfinella s
568	7	2.5	227	2	Q6BUE9	Q82j5 clostridium	641	7	2.5	251	1	ZNUC_ECOLI	P52648 escherichia
569	7	2.5	228	2	Q7VZN9	Q6bue9 debaryomyce	642	7	2.5	251	2	Q8Z5W6	Q8z5w6 salmonella
570	7	2.5	228	2	Q8ETU3	Q7vzn9 pyrochloroco	643	7	2.5	251	2	Q89GM2	Q89gm2 bradyrhizob
571	7	2.5	229	2	Q883F0	Q8etu3 oceanobacil	644	7	2.5	251	2	Q89QE2	Q89qe2 bradyrhizob
572	7	2.5	230	2	Q97414	Q883f0 pseudomonas	645	7	2.5	251	2	Q8G582	Q8g582 bifidobacte
573	7	2.5	230	2	Q7P6R9	Q97414 sulfolobus	646	7	2.5	251	2	Q9RY19	Q9ry19 deinococcus
574	7	2.5	230	2	Q65K67	Q7p6r9 fusobacteri	647	7	2.5	251	2	Q83KR7	Q83kr7 shigella fl
575	7	2.5	230	2	Q31711	Q65k67 bacillus li	648	7	2.5	252	2	O6LI01	O6li01 photobacter
576	7	2.5	230	2	Q8NVX0	O31711 bacillus su	649	7	2.5	252	2	Q6MGW2	O6mgw2 bdellovibri
577	7	2.5	230	2	Q6G8B6	Q8nvx0 staphylococ	650	7	2.5	252	2	Q6MPE0	O6mpe0 bdellovibri
578	7	2.5	231	2	Q6GVN5	Q6g8b6 staphylococ	651	7	2.5	252	2	Q6D4A8	Q6d4a8 erwinia car
579	7	2.5	231	2	Q98W31	Q8gvn5 mycobacteri	652	7	2.5	253	1	PSTB_PYRAB	Q9uz7 pyrococcus
580	7	2.5	231	2	Q73S69	Q98w31 rhizobium l	653	7	2.5	253	1	PSTB_PYRPU	Q8u242 pyrococcus
581	7	2.5	231	2	Q89EU1	Q73s69 mycobacteri	654	7	2.5	253	2	Q66AT7	Q66at7 versinia ps
582	7	2.5	232	2	O8UJE2	Q89eu1 bradyrhizob	655	7	2.5	253	2	Q82EU3	Q8zeu3 versinia pe
583	7	2.5	232	2	Q8YVM7	Q8yje2 agrobacteri	656	7	2.5	253	2	Q99WR6	Q99wr6 staphylococ
584	7	2.5	232	2	Q74LK0	Q8yvm7 anabaena sp	657	7	2.5	253	2	Q740F8	Q740f8 mycobacteri
585	7	2.5	233	2	Q7P429	Q74lk0 lactobacill	658	7	2.5	254	2	Q83189	Q83189 tropheryma
586	7	2.5	233	2	Q7P429	Q7p429 fusobacteri	659	7	2.5	254	2	Q8TN15	Q8tn15 methanosarc
587	7	2.5	233	2	Q7DBB3	Q7dbb3 neisseria m	660	7	2.5	254	2	Q8TR44	Q8tr44 methanosarc
588	7	2.5	233	2	Q9JRA3	Q9jra3 neisseria m	661	7	2.5	254	2	O9YDJ4	O9yjd4 aeropyrum p
589	7	2.5	234	2	Q70824	Q70824 hepatitis c	662	7	2.5	254	2	Q7MM92	Q7mw92 porphyromon
590	7	2.5	234	2	Q70825	Q70825 hepatitis c	663	7	2.5	254	2	Q8ESF4	Q8esf4 oceanobacil
591	7	2.5	234	2	Q70826	Q70826 hepatitis c	664	7	2.5	254	2	Q81585	Q81585 hepatitis c
592	7	2.5	234	2	Q70827	Q70827 hepatitis c	665	7	2.5	255	2	Q97WA2	Q97wa2 sulfolobus
593	7	2.5	234	2	Q70828	Q70828 hepatitis c	666	7	2.5	255	2	O33189	O33189 mycobacteri
594	7	2.5	234	2	Q70829	Q70829 hepatitis c	667	7	2.5	255	2	Q99TU0	Q99tu0 staphylococ
595	7	2.5	234	2	Q70830	Q70830 hepatitis c	668	7	2.5	255	2	Q7A0S6	Q7a0s6 staphylococ
596	7	2.5	234	2	Q70831	Q70831 hepatitis c	669	7	2.5	255	2	Q7A5D3	Q7a5d3 staphylococ
597	7	2.5	234	2	Q70832	Q70832 hepatitis c	670	7	2.5	255	2	Q7TZS5	Q7tzs5 mycobacteri
598	7	2.5	234	2	Q70833	Q70833 hepatitis c	671	7	2.5	256	2	Q8TKF8	Q8tkf8 methanosarc
599	7	2.5	234	2	Q70834	Q70834 hepatitis c	672	7	2.5	256	2	Q8KAQ1	Q8kaq1 chlorobium
600	7	2.5	234	2	Q70835	Q70835 hepatitis c	673	7	2.5	256	2	Q6N4P3	O6n4p3 rhodopseudo
601	7	2.5	234	2	Q70836	Q70836 hepatitis c	674	7	2.5	256	2	Q73Q19	Q73q19 treponema d
602	7	2.5	234	2	Q70837	Q70837 hepatitis c	675	7	2.5	257	1	LIVG_METJA	Q58663 methanococc
603	7	2.5	234	2	Q70838	Q70838 hepatitis c	676	7	2.5	257	1	ORC6_DROME	Q9ylb2 drosophila
604	7	2.5	234	2	Q70839	Q70839 hepatitis c	677	7	2.5	257	2	P71508	P71508 methylobact
605	7	2.5	234	2	Q70841	Q70841 hepatitis c	678	7	2.5	257	2	Q63CM2	Q63cm2 bacillus ce
606	7	2.5	234	2	Q70842	Q70842 hepatitis c	679	7	2.5	257	2	Q8XWN5	Q8xwn5 ralstonia s
607	7	2.5	234	2	O89253	O89253 hepatitis c	680	7	2.5	257	2	Q739X6	Q739x6 bacillus ce
608	7	2.5	234	2	O89254	O89254 hepatitis c	681	7	2.5	257	2	Q81RV4	Q81rv4 bacillus an
609	7	2.5	234	2	O89255	O89255 hepatitis c	682	7	2.5	257	2	Q6HK27	Q6hk27 bacillus th
610	7	2.5	234	2	O89256	O89256 hepatitis c	683	7	2.5	258	2	Q9HS04	Q9hs04 halobacteri
611	7	2.5	235	2	O8TWT8	Q8twt8 methanopyru	684	7	2.5	259	2	O6CFI6	O6cfi6 varrowia li
612	7	2.5	235	2	Q98LR7	Q98lr7 rhizobium l	685	7	2.5	259	2	Q6REJ2	Q6rej2 fusobacteri
613	7	2.5	236	2	Q9YDJ2	Q9yjd2 aeropyrum p	686	7	2.5	259	2	Q6FFL0	Q6ffl0 acinetobact
614	7	2.5	237	2	Q9YDJ2	P57403 buchnera ap	687	7	2.5	259	2	Q6ADG4	Q6adg4 leifsonia x
615	7	2.5	238	1	ZNUC_BUCAI	Q8k9m6 buchnera ap	688	7	2.5	260	2	O57872	O57872 pyrococcus

Q89aj0 buchnera ap	Q89aj0 buchnera ap
Q860k6 tragalaphus	Q860k6 tragalaphus
Q9wx8 thermotoga	Q9wx8 thermotoga
O18131 caenorhabdi	O18131 caenorhabdi
Q2dl2 listeria in	Q2dl2 listeria in
Q8n749 rhodopseudo	Q8n749 rhodopseudo
Q6dia9 erwinia car	Q6dia9 erwinia car
Q6up75 alcaligenes	Q6up75 alcaligenes
Q8rir9 fusobacteri	Q8rir9 fusobacteri
Q87jt5 vibrio para	Q87jt5 vibrio para
Q7dm58 arabidopsis	Q7dm58 arabidopsis
Q8m391 corynebacte	Q8m391 corynebacte
Q8lx89 bacillus an	Q8lx89 bacillus an
P46903 bacillus su	P46903 bacillus su
Q6mlx6 bdellovibri	Q6mlx6 bdellovibri
Q8zvx1 pyrobaculum	Q8zvx1 pyrobaculum
Q8lep0 bacillus ce	Q8lep0 bacillus ce
Q6fll1 mesoplasma	Q6fll1 mesoplasma
Q829v5 streptomyce	Q829v5 streptomyce
Q8gev2 methylobact	Q8gev2 methylobact
Q8nn48 corynebacte	Q8nn48 corynebacte
O8uje3 agrobacteri	O8uje3 agrobacteri
Q6n2l3 rhodopseudo	Q6n2l3 rhodopseudo
Q748l6 geobacter s	Q748l6 geobacter s
Q7map5 wolfinella s	Q7map5 wolfinella s
P52648 escherichia	P52648 escherichia
Q8z5w6 salmonella	Q8z5w6 salmonella
Q89gm2 bradyrhizob	Q89gm2 bradyrhizob
Q89qe2 bradyrhizob	Q89qe2 bradyrhizob
Q8g582 bifidobacte	Q8g582 bifidobacte
Q9ry19 deinococcus	Q9ry19 deinococcus
Q83kr7 shigella fl	Q83kr7 shigella fl
O6li01 photobacter	O6li01 photobacter
O6mgw2 bdellovibri	O6mgw2 bdellovibri
O6mpe0 bdellovibri	O6mpe0 bdellovibri
Q6d4a8 erwinia car	Q6d4a8 erwinia car
Q9uz7 pyrococcus	Q9uz7 pyrococcus
Q8u242 pyrococcus	Q8u242 pyrococcus
Q66at7 versinia ps	Q66at7 versinia ps
Q8zeu3 versinia pe	Q8zeu3 versinia pe
Q99wr6 staphylococ	Q99wr6 staphylococ
Q740f8 mycobacteri	Q740f8 mycobacteri
Q83189 tropheryma	Q83189 tropheryma
Q8tn15 methanosarc	Q8tn15 methanosarc
Q8tr44 methanosarc	Q8tr44 methanosarc
O9yjd4 aeropyrum p	O9yjd4 aeropyrum p
Q7mw92 porphyromon	Q7mw92 porphyromon
Q8esf4 oceanobacil	Q8esf4 oceanobacil
Q81585 hepatitis c	Q81585 hepatitis c
Q97wa2 sulfolobus	Q97wa2 sulfolobus
O33189 mycobacteri	O33189 mycobacteri
Q99tu0 staphylococ	Q99tu0 staphylococ
Q7a0s6 staphylococ	Q7a0s6 staphylococ
Q7a5d3 staphylococ	Q7a5d3 staphylococ
Q7tzs5 mycobacteri	Q7tzs5 mycobacteri
Q8tkf8 methanosarc	Q8tkf8 methanosarc
Q8kaq1 chlorobium	Q8kaq1 chlorobium
O6n4p3 rhodopseudo	O6n4p3 rhodopseudo
Q73q19 treponema d	Q73q19 treponema d
Q58663 methanococc	Q58663 methanococc
Q9ylb2 drosophila	Q9ylb2 drosophila
P71508 methylobact	P71508 methylobact
Q63cm2 bacillus ce	Q63cm2 bacillus ce
O8xwn5 ralstonia s	O8xwn5 ralstonia s
Q739x6 bacillus ce	Q739x6 bacillus ce
Q81rv4 bacillus an	Q81rv4 bacillus an
Q6hk27 bacillus th	Q6hk27 bacillus th
Q9hs04 halobacteri	Q9hs04 halobacteri
O6cfi6 varrowia li	O6cfi6 varrowia li
Q8rej2 fusobacteri	Q8rej2 fusobacteri
Q6ffl0 acinetobact	Q6ffl0 acinetobact
Q6adg4 leifsonia x	Q6adg4 leifsonia x
O57872 pyrococcus	O57872 pyrococcus

689	7	2.5	260	2	Q8U4L3	Q8u4l3 pyrococcus	762	7	2.5	281	2	Q9ZIC9	Q9zic9 listeria mo
690	7	2.5	260	2	Q01842	Q01842 caenorhabdi	763	7	2.5	281	2	Q9PKJ1	Q9pkj1 chlamydia m
691	7	2.5	260	2	Q62IC1	Q62ic1 burkholderi	764	7	2.5	281	2	Q6AFU1	Q6afu1 leifsonia x
692	7	2.5	260	2	Q63WF1	Q63wf1 burkholderi	765	7	2.5	282	2	Q8VIM1	Q8vim1 mus musculus
693	7	2.5	260	2	Q8RIR8	Q8rir8 fusobacteri	766	7	2.5	282	2	Q7TPU2	Q7tpu2 mus musculus
694	7	2.5	260	2	Q8RKC6	Q8rkcs streptomyce	767	7	2.5	283	2	Q87CB3	Q87cb3 xylella fas
695	7	2.5	261	2	Q26555	Q26555 methanobact	768	7	2.5	283	2	Q89F04	Q89f04 bradyrhizob
696	7	2.5	261	2	Q9R6G1	Q9r6g1 agrobacteri	769	7	2.5	283	2	Q9PD02	Q9pd02 xylella fas
697	7	2.5	261	2	Q9RGL9	Q9rgl9 staphylococ	770	7	2.5	284	1	Y46B_MYCPN	Y50316 mycoplasma
698	7	2.5	261	2	Q9RQC6	Q9rqc6 zymomonas m	771	7	2.5	284	2	O59479	O59479 pyrococcus
699	7	2.5	261	2	Q98GB7	Q98gb7 rhizobium l	772	7	2.5	284	2	O87316	O87316 mycobacteri
700	7	2.5	261	2	Q6G910	Q6g910 staphylococ	773	7	2.5	284	2	Q9K245	Q9k245 chlamydia p
701	7	2.5	261	2	Q6GGE3	Q6g9e3 staphylococ	774	7	2.5	284	2	Q9Z8Y3	Q9z8y3 chlamydia p
702	7	2.5	261	2	Q8UB01	Q8ub01 agrobacteri	775	7	2.5	284	2	Q81589	Q81589 hepatitis c
703	7	2.5	262	2	Q67RE7	Q67re7 symbiobacte	776	7	2.5	285	1	PANC_CAUCR	Q9a6c8 caulobacter
704	7	2.5	262	2	Q82HA2	Q82ha2 streptomyce	777	7	2.5	287	2	Q8PV82	Q8pv82 methanosarc
705	7	2.5	262	2	Q8DYG6	Q8dyg6 streptococc	778	7	2.5	287	2	O6MMA8	O6mma8 bdellovibri
706	7	2.5	262	2	Q8E429	Q8e429 streptococc	779	7	2.5	287	2	O8EUF1	O8euf1 mycoplasma
707	7	2.5	263	2	Q8TM86	Q8tm86 methanosarc	780	7	2.5	288	2	O6XYZ4	O6xyz4 spiroplasma
708	7	2.5	263	2	Q8TRZ0	Q8trz0 methanosarc	781	7	2.5	288	2	Q82ZS5	Q82zs5 chlamydophi
709	7	2.5	263	2	Q8CSE1	Q8cse1 staphylococ	782	7	2.5	288	2	Q82G37	Q82g37 streptomyce
710	7	2.5	263	2	Q8CP24	Q8cp24 pasteurella	783	7	2.5	289	1	STAR_XENLA	Q9dgo8 xenopus lae
711	7	2.5	264	2	Q8UC28	Q8uc28 agrobacteri	784	7	2.5	289	2	O6NHR4	O6nhr4 corynebacte
712	7	2.5	265	2	Q7N545	Q7n545 photorhabdu	785	7	2.5	289	2	O89G67	O89g67 bradyrhizob
713	7	2.5	266	2	Q7QM49	Q7qm49 anopheles g	786	7	2.5	289	2	Q9KZV3	Q9kzv3 streptomyce
714	7	2.5	266	2	Q8XIK5	Q8xyk5 raistonia s	787	7	2.5	290	2	Q7V156	Q7v156 helicobacte
715	7	2.5	266	2	Q9WY65	Q9wy65 thermotoga	788	7	2.5	291	2	Q87VMO	Q87vm0 pseudomonas
716	7	2.5	266	2	Q8UBX4	Q8ubx4 agrobacteri	789	7	2.5	291	2	O88DG1	O88dg1 pseudomonas
717	7	2.5	268	1	ZNUC_HAEIN	P44692 haemophilus	790	7	2.5	292	2	O84BI7	O84bi7 streptococc
718	7	2.5	268	2	Q8ZNV7	Q8znv7 salmonella	791	7	2.5	292	2	O34641	O34641 bacillus su
719	7	2.5	269	2	Q8XYT0	Q8xyt0 spiroplasma	792	7	2.5	292	2	O6MKT3	O6mkt3 bdellovibri
720	7	2.5	269	2	Q8NVB5	Q8nvb5 staphylococ	793	7	2.5	292	2	Q72HG0	Q72hg0 thermus the
721	7	2.5	269	2	Q9S847	Q9s847 staphylococ	794	7	2.5	293	2	Q8NR37	Q8nr37 corynebacte
722	7	2.5	269	2	Q7A470	Q7a470 staphylococ	795	7	2.5	293	2	O8R7Y4	O8r7y4 thermoanaer
723	7	2.5	269	2	Q8CRI6	Q8cri6 staphylococ	796	7	2.5	293	2	O8DT43	O8dt43 streptococc
724	7	2.5	269	2	Q6G799	Q6g799 staphylococ	797	7	2.5	294	2	O9XCW9	O9xcw9 rhodobacter
725	7	2.5	269	2	Q6GEL3	Q6gel3 staphylococ	798	7	2.5	294	2	O9PPV1	O9ppv1 ureaplasma
726	7	2.5	270	2	Q630M0	Q630m0 bacillus ce	799	7	2.5	296	2	Q67LV2	Q67lv2 symbiobacte
727	7	2.5	270	2	Q72X68	Q72x68 bacillus ce	800	7	2.5	297	2	O9CNM8	O9cnm8 pasteurella
728	7	2.5	270	2	Q814P3	Q814p3 bacillus ce	801	7	2.5	298	2	O886U8	O886u8 pseudomonas
729	7	2.5	270	2	O81J80	O81j80 bacillus an	802	7	2.5	299	2	O68479	O68479 achromobact
730	7	2.5	270	2	O6HAQ5	O6haq5 bacillus th	803	7	2.5	299	2	O9R9K7	O9r9k7 pyrococcus
731	7	2.5	271	2	Q8X470	Q8x470 streptomyce	804	7	2.5	299	2	Q7SL01	Q7sl01 human immun
732	7	2.5	271	2	Q8JRV1	Q8jrv1 phthorimaea	805	7	2.5	301	2	Q8TDQ0	Q8tdq0 homo sapien
733	7	2.5	272	2	Q9EX40	Q9ex40 streptomyce	806	7	2.5	301	2	Q96K94	Q96k94 homo sapien
734	7	2.5	273	2	Q913S2	Q913s2 anabaena sp	807	7	2.5	302	2	Q69WA8	Q69wa8 oryza sativ
735	7	2.5	273	2	Q8RCQ9	Q8rcq9 thermoanaer	808	7	2.5	302	2	O55096	O55096 synchocyst
736	7	2.5	274	1	Y179_MYCGR	P47425 mycoplasma	809	7	2.5	302	2	O6SFX4	O6sfx4 uncultured
737	7	2.5	274	1	Y179_MYCPN	Q50294 mycoplasma	810	7	2.5	302	2	O8D2S4	O8d2s4 wiggleswort
738	7	2.5	274	2	Q7QMR0	Q7qmr0 anopheles g	811	7	2.5	302	2	O57067	O57067 hepatitis c
739	7	2.5	274	2	Q7T517	Q7t517 cryptophleb	812	7	2.5	303	2	Q74D18	Q74d18 geobacter s
740	7	2.5	275	2	Q82E94	Q82e94 streptomyce	813	7	2.5	303	2	Q7N873	Q7n873 photorhabdu
741	7	2.5	275	2	O83FW1	O83fw1 tropheryma	814	7	2.5	304	2	O9AQ20	O9aq20 bradyrhizob
742	7	2.5	275	2	O8SGJ1	O8sgj1 bradyrhizob	815	7	2.5	304	2	O82SG0	O82sg0 nitrosomona
743	7	2.5	276	2	Q988C7	Q988c7 rhizobium l	816	7	2.5	304	2	O83D12	O83d12 coxiella bu
744	7	2.5	276	2	Q9X8G3	Q9x8g3 streptomyce	817	7	2.5	305	2	O6ML88	O6ml88 bdellovibri
745	7	2.5	277	2	Q7D2U3	Q7d2u3 agrobacteri	818	7	2.5	305	2	Q72RE2	Q72re2 leptospira
746	7	2.5	277	2	O84204	O84204 chlamydia t	819	7	2.5	305	2	O87LU7	O87lu7 vibrio para
747	7	2.5	278	1	BJTJ_ECOLI	P77277 escherichia	820	7	2.5	305	2	Q8F4C7	Q8f4c7 leptospira
748	7	2.5	278	2	Q66S28	Q66s28 oikopleura	821	7	2.5	305	2	O9KUD3	O9kud3 vibrio chol
749	7	2.5	278	2	Q8FF96	Q8ff96 escherichia	822	7	2.5	305	2	O8VIM2	O8vim2 mus musculu
750	7	2.5	278	2	Q8XBH0	Q8xbh0 escherichia	823	7	2.5	306	2	Q82K72	Q82k72 burkholderi
751	7	2.5	278	2	Q86826	Q86826 hepatitis c	824	7	2.5	306	2	Q63TX3	Q63tx3 burkholderi
752	7	2.5	279	1	BJTJ_SALTY	P41794 salmonella	825	7	2.5	306	2	O98DQ6	O98dq6 rhizobium l
753	7	2.5	279	2	O8Y454	O8y454 listeria mo	826	7	2.5	306	2	O6N432	O6n432 rhodospseudo
754	7	2.5	279	2	Q927N8	Q927n8 listeria in	827	7	2.5	306	2	O7UJ07	O7uj07 rhodopirell
755	7	2.5	279	2	Q97JB8	Q97jb8 clostridium	828	7	2.5	306	2	O9S288	O9s288 streptomyce
756	7	2.5	279	2	Q71WH7	Q71wn7 listeria mo	829	7	2.5	307	2	Q7MHV1	Q7mhv1 vibrio vuln
757	7	2.5	279	2	Q74JK2	Q74jk2 lactobacill	830	7	2.5	307	2	Q7VWM9	Q7vwm9 bordetella
758	7	2.5	279	2	Q8ETV7	Q8etv7 oceanobacil	831	7	2.5	307	2	Q7WH89	Q7wh89 bordetella
759	7	2.5	280	1	CBIO_METTH	O26236 methanobact	832	7	2.5	307	2	O89FX1	O89fx1 bradyrhizob
760	7	2.5	280	2	Q9V1Q4	Q9v1q4 pyrococcus	833	7	2.5	307	2	O8DC14	O8dc14 vibrio vuln
761	7	2.5	281	2	Q67MB5	Q67mb5 symbiobacte	834	7	2.5	307	2	O9HXW8	O9hwx8 pseudomonas

Q9zic9 listeria mo	Q9pkj1 chlamydia m	Q6afu1 leifsonia x	Q8vim1 mus musculu	Q7tpu2 mus musculu	Q87cb3 xylella fas	Q89f04 bradyrhizob	Q9pd02 xylella fas	Y50316 mycoplasma	O59479 pyrococcus	O87316 mycobacteri	Q9k245 chlamydia p	Q9z8y3 chlamydia p	Q81589 hepatitis c	Q9a6c8 caulobacter	Q8pv82 methanosarc	O6mma8 bdellovibri	O8euf1 mycoplasma	O6xyz4 spiroplasma	Q82zs5 chlamydophi	Q82g37 streptomyce	Q9dgo8 xenopus lae	O6nhr4 corynebacte	O89g67 bradyrhizob	Q9kzv3 streptomyce	Q7v156 helicobacte	Q87vm0 pseudomonas	O88dg1 pseudomonas	O84bi7 streptococc	O34641 bacillus su	O6mkt3 bdellovibri	Q72hg0 thermus the	Q8nr37 corynebacte	O8r7y4 thermoanaer	O8dt43 streptococc	O9xcw9 rhodobacter	O9ppv1 ureaplasma	Q67lv2 symbiobacte	O9cnm8 pasteurella	O886u8 pseudomonas	O68479 achromobact	O9r9k7 pyrococcus	O7sl01 human immun	Q8tdq0 homo sapien	Q96k94 homo sapien	Q69wa8 oryza sativ	O55096 synchocyst	O6sfx4 uncultured	O8d2s4 wiggleswort	O57067 hepatitis c	Q74d18 geobacter s	Q7n873 photorhabdu	O9aq20 bradyrhizob	O82sg0 nitrosomona	O83d12 coxiella bu	O6ml88 bdellovibri	Q72re2 leptospira	O87lu7 vibrio para	Q8f4c7 leptospira	O9kud3 vibrio chol	O8vim2 mus musculu	Q82k72 burkholderi	Q63tx3 burkholderi	O98dq6 rhizobium l	O6n432 rhodospseudo	O7uj07 rhodopirell	O9s288 streptomyce	Q7mhv1 vibrio vuln	Q7vwm9 bordetella	Q7wh89 bordetella	O89fx1 bradyrhizob	O8dc14 vibrio vuln	O9hwx8 pseudomonas
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835	7	2.5	307	2	O54947	O54947 rattus norv	908	7	2.5	318	2	Q47072	Q47072 escherichia
836	7	2.5	308	1	YADG_ECOLI	P36879 escherichia	909	7	2.5	318	2	Q8G3S7	Q8G3S7 bifidobacte
837	7	2.5	308	1	YEHX_ECOLI	P33360 escherichia	910	7	2.5	319	1	FMT_LACLA	Q9ce9 lactococcus
838	7	2.5	308	2	Q93E11	P93e11 rhizobium l	911	7	2.5	319	1	OPPF_LACLA	Q07734 lactococcus
839	7	2.5	308	2	Q66EG8	Q66eg8 yersinia ps	912	7	2.5	319	2	Q8DH4	Q8dh4p4 synechococ
840	7	2.5	308	2	Q70D22	Q70dz2 ruminococu	913	7	2.5	320	1	FLIG_BUCBP	Q89az9 buchnera ap
841	7	2.5	308	2	Q829D7	Q8z9d7 salmonella	914	7	2.5	320	2	Q8ZXG5	Q8zxg5 pyrobaculum
842	7	2.5	308	2	Q82BK3	Q8z2b3 yersinia pe	915	7	2.5	320	2	Q8RCR0	Q8rcr0 thermoanaer
843	7	2.5	308	2	Q82BK3	Q8z2b3 yersinia pe	916	7	2.5	321	2	Q8Y317	Q8y317 ralstonia s
844	7	2.5	308	2	Q82RR9	Q8zrr9 salmonella	917	7	2.5	322	2	Q8U4P5	Q8u4p5 pyrococcus
845	7	2.5	308	2	Q92P94	Q92p94 rhizobium m	918	7	2.5	322	2	Q8ZTD0	Q8ztd0 pyrobaculum
846	7	2.5	308	2	Q982D0	Q982d0 rhizobium l	919	7	2.5	322	2	Q6NHB9	Q6nib9 corynebacte
847	7	2.5	308	2	Q98DW2	Q98dw2 rhizobium l	920	7	2.5	323	2	Q9V2C9	Q9v2c9 pyrococcus
848	7	2.5	308	2	Q83T83	Q83t83 salmonella	921	7	2.5	324	2	Q99TV0	Q99tv0 streptomyce
849	7	2.5	308	2	Q87M31	Q87m31 vibrio para	922	7	2.5	324	2	Q7A0T0	Q7a0t0 staphylococ
850	7	2.5	308	2	Q8FFW4	Q8ffw4 escherichia	923	7	2.5	324	2	Q7A5E1	Q7a5e1 staphylococ
851	7	2.5	308	2	Q8FL36	Q8fl36 escherichia	924	7	2.5	324	2	Q9S2S8	Q9s2s8 streptomyce
852	7	2.5	308	2	Q8UE54	Q8ue54 agrobacteri	925	7	2.5	324	2	Q6G922	Q6g922 staphylococ
853	7	2.5	308	2	Q8X4M3	Q8x4m3 escherichia	926	7	2.5	324	2	Q6GGF5	Q6ggf5 staphylococ
854	7	2.5	308	2	Q8X4V8	Q8x4v8 escherichia	927	7	2.5	325	2	Q7RG45	Q7rg45 plasmodium
855	7	2.5	308	2	Q83ME8	Q83me8 shigella fl	928	7	2.5	325	2	Q65TN7	Q65tn7 manheimia
856	7	2.5	308	2	Q83KF9	Q83kf9 shigella fl	929	7	2.5	325	2	Q8S875	Q8s875 thermoanaer
857	7	2.5	309	2	Q8S2J2	Q8s2j2 streptomyce	930	7	2.5	326	1	YGBR_ECOLI	P52052 escherichia
858	7	2.5	310	2	Q87E26	Q87e26 xylella fas	931	7	2.5	326	2	O30385	O30385 myxococcus
859	7	2.5	310	2	Q87VE5	Q87ve5 pseudomonas	932	7	2.5	326	2	O85249	O85249 thermotoga
860	7	2.5	310	2	Q86LN4	Q86ln4 pseudomonas	933	7	2.5	326	2	Q823G7	Q823g7 chlamydophi
861	7	2.5	310	2	Q891I5	Q891i5 bradyrhizob	934	7	2.5	327	2	Q875H5	Q875h5 trichoderma
862	7	2.5	310	2	Q91O31	Q91o31 pseudomonas	935	7	2.5	327	2	Q92ML5	Q92ml5 rhizobium m
863	7	2.5	311	1	FMT_STRPN	Q97pa6 streptococ	936	7	2.5	327	2	Q8CP28	Q8cp28 staphylococ
864	7	2.5	311	1	FMT_STR6	Q8dar7 streptococ	937	7	2.5	327	2	Q9F2X6	Q9f2x6 streptomyce
865	7	2.5	311	1	LUCI_RENRE	P27652 renilla ren	938	7	2.5	328	1	YDDP_ECOLI	P77268 escherichia
866	7	2.5	311	1	LUCI_RENRE	P27652 renilla ren	939	7	2.5	328	2	Q8XAT9	Q8xat9 escherichia
867	7	2.5	311	2	Q939R7	Q939r7 streptococ	940	7	2.5	328	2	O83KV6	Q83kv6 shigella fl
868	7	2.5	311	2	Q8Y966	Q8y966 listeria mo	941	7	2.5	328	2	Q9EC34	Q9ec34 human immun
869	7	2.5	311	2	Q92DY9	Q92dy9 listeria in	942	7	2.5	328	2	Q9EDH2	Q9edh2 human immun
870	7	2.5	311	2	Q722M8	Q722m8 listeria mo	943	7	2.5	328	2	Q9EEM7	Q9eem7 human immun
871	7	2.5	311	2	Q741A8	Q741a8 mycobacteri	944	7	2.5	328	2	Q9EGG1	Q9egg1 human immun
872	7	2.5	311	2	Q82264	Q82264 enterococu	945	7	2.5	328	2	Q9EGT5	Q9egt5 human immun
873	7	2.5	312	2	Q66D11	Q66d11 yersinia ps	946	7	2.5	328	2	Q9E172	Q9e172 human immun
874	7	2.5	312	2	Q66D11	Q66d11 yersinia ps	947	7	2.5	328	2	Q9EIG3	Q9eig3 human immun
875	7	2.5	312	2	Q62GT1	Q62gt1 yersinia pe	948	7	2.5	328	2	Q9EJ38	Q9ej38 human immun
876	7	2.5	312	2	Q6LMJ3	Q6lmj3 photobacter	949	7	2.5	328	2	Q9EJD3	Q9ejd3 human immun
877	7	2.5	312	2	Q8EAU0	Q8eau0 shewanella	950	7	2.5	328	2	Q9EJT6	Q9ejt6 human immun
878	7	2.5	312	2	Q9CNG2	Q9cng2 pasteurella	951	7	2.5	328	2	Q9EJV0	Q9ejv0 human immun
879	7	2.5	312	2	Q6D1X2	Q6dlx2 erwinnia car	952	7	2.5	328	2	Q9EJW0	Q9ejw0 human immun
880	7	2.5	312	2	Q8UIU5	Q8uius agrobacteri	953	7	2.5	328	2	Q9EKC7	Q9ekc7 human immun
881	7	2.5	313	2	Q7S787	Q7s787 neurospora	954	7	2.5	328	2	Q9EKK6	Q9ekk6 human immun
882	7	2.5	313	2	Q6B6P8	Q6b6p8 azospirillu	955	7	2.5	330	2	Q72NZ3	Q72nz3 leptospira
883	7	2.5	313	2	O53149	O53149 mycobacteri	956	7	2.5	330	2	Q8F7H6	Q8f7h6 leptospira
884	7	2.5	313	2	Q7U014	Q7u014 acinetobact	957	7	2.5	330	2	Q9WKN5	Q9wxn5 thermotoga
885	7	2.5	313	2	Q7U014	Q7u014 mycobacteri	958	7	2.5	331	2	Q46780	Q46780 escherichia
886	7	2.5	313	2	Q894X8	Q894x8 clostridium	959	7	2.5	331	2	Q8PFB7	Q8pfb7 xanthomonas
887	7	2.5	313	2	Q6ZYK0	Q6zyk0 pyrobaculum	960	7	2.5	331	2	Q7W9H3	Q7w9h3 bordetella
888	7	2.5	314	2	Q9HLG2	Q9hlq2 thermoplasm	961	7	2.5	331	2	Q82BK2	Q82bk2 streptomyce
889	7	2.5	314	2	Q9UZ25	Q9uz25 pyrococcus	962	7	2.5	331	2	Q9WXR4	Q9wxr4 thermotoga
890	7	2.5	314	2	Q9ATD0	Q9atd0 gossypium h	963	7	2.5	332	2	Q8P3U2	Q8p3u2 xanthomonas
891	7	2.5	314	2	Q8P4P7	Q8p4p7 xanthomonas	964	7	2.5	333	2	O8Y843	O8y843 listeria mo
892	7	2.5	314	2	Q8PGB7	Q8pgb7 xanthomonas	965	7	2.5	334	1	GP12_MOUSE	P35412 mus musculus
893	7	2.5	314	2	Q82A38	Q82a38 streptomyce	966	7	2.5	334	1	GP12_RAT	P30951 rattus norv
894	7	2.5	314	2	Q9A333	Q9a333 caulobacter	967	7	2.5	334	2	Q8VQK7	Q8vqk7 brucella ab
895	7	2.5	315	2	Q97WF8	Q97wf8 sulfolobus	968	7	2.5	334	2	Q9ABN8	Q9abn8 caulobacter
896	7	2.5	315	2	Q8XER9	Q8xer9 salmonella	969	7	2.5	335	1	Y7I9_ANASP	Y7i9 anabaena sp
897	7	2.5	315	2	Q49707	Q49707 mycobacteri	970	7	2.5	335	2	O66E43	O66e43 yersinia ps
898	7	2.5	315	2	Q7CQ89	Q7cq89 salmonella	971	7	2.5	335	2	Q9LCC9	Q9lcc9 ochrobactru
899	7	2.5	315	2	Q9PCW0	Q9pcw0 xylella fas	972	7	2.5	335	2	Q92CV8	Q92cv8 listeria in
900	7	2.5	315	2	Q8JAD6	Q8jad6 human immun	973	7	2.5	335	2	Q720Z5	Q720z5 listeria mo
901	7	2.5	316	1	YCF9_YEAST	P25586 saccharomyc	974	7	2.5	335	2	Q7N1L6	Q7n1l6 gloeobacter
902	7	2.5	316	2	Q97YF8	Q97yfp8 sulfolobus	975	7	2.5	335	2	O88RL5	O88rl5 pseudomonas
903	7	2.5	316	2	Q7P326	Q7p326 fusobacteri	976	7	2.5	335	2	Q8EQ18	Q8eq18 oceanobacil
904	7	2.5	316	2	Q8RII4	Q8rii4 fusobacteri	977	7	2.5	337	2	Q7U551	Q7u551 synechococ
905	7	2.5	316	2	Q9F3A8	Q9f3a8 streptomyce	978	7	2.5	337	2	Q7V639	Q7v639 prochloroco
906	7	2.5	317	2	O6N3A5	O6n3a5 rhodopsendo	979	7	2.5	337	2	Q7VDD4	Q7vdd4 prochloroco
907	7	2.5	317	2	Q7V215	Q7v215 prochloroco	980	7	2.5	337	2	Q8FT81	Q8ft81 corynebacte

981 7 2.5 338 2 Q6D122 Q6D122 erwinia car
 982 7 2.5 339 1 F16Q HUMAN O00757 homo sapien
 983 7 2.5 339 2 Q976N8 Q976N8 sulfolobus
 984 7 2.5 339 2 Q6F153 Q6F153 homo sapien
 985 7 2.5 339 2 Q9N0J6 Q9N0J6 oryctolagus
 986 7 2.5 339 2 Q8YBT4 Q8YBT4 bruceella me
 987 7 2.5 339 2 Q8YUH4 Q8YUH4 anabaena sp
 988 7 2.5 339 2 Q9IX26 Q9IX26 mus musculus
 989 7 2.5 339 2 Q9QXD7 Q9QXD7 mus musculus
 990 7 2.5 339 2 Q9Z1N1 Q9Z1N1 rattus norv
 991 7 2.5 340 1 GLS1 YERPE Q9Z1N1 rattus norv
 992 7 2.5 340 2 Q8N072 Q8N072 corynebacte
 993 7 2.5 340 2 Q9I9H7 Q9I9H7 zaccys dhum
 994 7 2.5 341 2 Q7UBN1 Q7UBN1 shigella fl
 995 7 2.5 341 2 Q8XC09 Q8XC09 escherichia
 996 7 2.5 342 2 Q7PU47 Q7PU47 anopheles g
 997 7 2.5 342 2 Q82DR3 Q82DR3 streptomyce
 998 7 2.5 343 1 METN YERPE Q82DR3 streptomyce
 999 7 2.5 343 2 Q657L9 Q657L9 yersinia ps
 1000 7 2.5 343 2 Q97NU4 Q97NU4 streptococc

ALIGNMENTS

RESULT 1
 Q97N51 ID Q97N51 PRELIMINARY; PRT; 279 AA.
 AC DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE ABC transporter, ATP-binding protein.
 GN OrderedLocusNames=SP2220;
 OS Streptococcus pneumoniae;
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus;
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC BAA-334 / TIGR4;
 RX MEDLINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217;
 RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S.N., Heidelberg J.F., DeBoy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M.L., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzapple E.K., Khouri H.M., Wolf A.M., Utterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S.V., Dickinson T.,
 RA Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.";
 RL Science 293:498-506(2001).
 CC -!- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; AE007509; AAK76268.1; --
 DR FIR; C95259; C95259.
 DR HSSP; P02915; 1B0U.
 DR TIGR; SP2220; --
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; P:ATP binding; IEA.
 DR GO; GO:0042626; P:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA ATPase.
 DR InterPro; IPR003439; ABC transporter.
 DR Pfam; PF00005; ABC tran; 1.
 DR ProDom; PD000006; ABC transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
 KW ATP-binding; Complete proteome.
 SQ SEQUENCE 279 AA; 30525 MW; E051E473D082AD32 CRC64;

Query Match 100.0%; Score 279; DB 2; Length 279;
 Best Local Similarity 100.0%; Pred. No. 2e-266;
 Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGIALENNVFTYQSGTTPLAGAALSDVSLTIEDSGSYTALIGHTGSGKSTILQLLNGLLVPS 60
 DB 1 MGIALENNVFTYQSGTTPLAGAALSDVSLTIEDSGSYTALIGHTGSGKSTILQLLNGLLVPS 60
 QY 61 QGSRVVRFTLTITSKNDIRQIRKQVGLVQFAENQIPRETVLKDVAFGPNFGVSEED 120
 DB 61 QGSRVVRFTLTITSKNDIRQIRKQVGLVQFAENQIPRETVLKDVAFGPNFGVSEED 120
 QY 121 AVKTAREKALVGVDESIFDRSPPELGGQRRVAIAGILAMEPAAILVLDPTAGLDPLG 180
 DB 121 AVKTAREKALVGVDESIFDRSPPELGGQRRVAIAGILAMEPAAILVLDPTAGLDPLG 180
 QY 181 RKEMLTFLFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKSPDVFDQVVFME 240
 DB 181 RKEMLTFLFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKSPDVFDQVVFME 240
 QY 241 EVQLGVPKITAFCKRLADRGVSPFKRLPIKIBEFKESLNG 279
 DB 241 EVQLGVPKITAFCKRLADRGVSPFKRLPIKIBEFKESLNG 279

RESULT 2

Q8DMY0 ID Q8DMY0 PRELIMINARY; PRT; 279 AA.
 AC DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein ABC-NBP.
 GN Name=ABC-NBP; OrderedLocusNames=spr2025;
 OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus;
 OX NCBI_TaxID=171101;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21429245; PubMed=11544234;
 RX DOI=10.1128/JB.183.19.5709-5717.2001;
 RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
 RA DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geisinger C.,
 RA Gilmour R., Glass J.S., Kuoja H., Kraft A.R., Lagace R.E.,
 RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
 RA McAhren S.M., McHenry M., McLeaster K., Mundy C.W., Nicas T.I.,
 RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rocky P.,
 RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
 RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostack P.R. Jr., Skatrud P.L.,
 RA Glass J.I.;
 RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
 RL J. Bacteriol. 183:5709-5717(2001).
 CC -!- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; AE008566; AAL00827.1; --
 DR FIR; F98124; F98124.
 DR HSSP; P02915; 1B0U.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; P:ATP binding; IEA.
 DR GO; GO:0042626; P:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA ATPase.
 DR InterPro; IPR003439; ABC transporter.
 DR Pfam; PF00005; ABC tran; 1.
 DR ProDom; PD000006; ABC transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
 KW ATP-binding; Complete proteome.
 SQ SEQUENCE 279 AA; 30553 MW; FBSA148C367A6032 CRC64;

Query Match 59.9%; Score 167; DB 2; Length 279;


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Best Local Similarity 99.6%; Pred. No. 6.8e-156;
Matches 267; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 YQGTPLASALSDVSLTIEDSGSYTALIGHTSGKSTIQLLNGLLVPSQGSVRVFDTLI 71
DB 12 YQGTPLASALSDVSLTIEDSGSYTALIGHTSGKSTIQLLNGLLVPSQGSVRVFDTLI 71
QY 72 TSTSNKKDIQIRKQVGLVQFAENQIPEETVLKDVAFGPQNGFVSEEDAVKTAREKAL 131
DB 72 TSTSNKKDIQIRKQVGLVQFAENQIPEETVLKDVAFGPQNGFVSEEDAVKTAREKAL 131
QY 132 VGIDSLFDRSPFELSGGQRRVATAGILAMEPAILVLDEPTAGLDPLGRKELMTLFFKKL 191
DB 132 VGIDSLFDRSPFELSGGQRRVATAGILAMEPAILVLDEPTAGLDPLGRKELMTLFFKKL 191
QY 192 HQSGMTIVLTHLMDVDAFYANQVYMEKGRVLKGGKPSDVFQDVVFMEVQLGVPKITA 251
DB 192 HQSGMTIVLTHLMDVDAFYANQVYMEKGRVLKGGKPSDVFQDVVFMEVQLGVPKITA 251
QY 252 FCKRLADRGVSKRLPIKIEEKESLNG 279
DB 252 FCKRLADRGVSKRLPIKIEEKESLNG 279

RESULT 3
Q9CIS8 PRELIMINARY; PRT; 288 AA.
AC Q9CIS8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABC transporter ATP-binding protein.
GN Name=yche; OrderedLocNames=Li0278;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1L1403;
RX MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr.1697R;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE06265; AAK04376.1; --
DR PIR; F8659; F8659.
DR HSSP; P58301; IUS8.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Complete proteome.
KW SEQUENCE 288 AA; 31848 MW; 9326C417DE7AEF22 CRC64;
SQ SEQUENCE FROM N.A.
RC STRAIN=1L1403;
RX MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr.1697R;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE06265; AAK04376.1; --
DR PIR; F8659; F8659.
DR HSSP; P58301; IUS8.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Complete proteome.
KW SEQUENCE 288 AA; 31848 MW; 9326C417DE7AEF22 CRC64;
SQ
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Query Match 8.2%; Score 23; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 SPFELSGGQRRVATAGILAMEP 164
DB 141 SPFELSGGQRRVATAGILAMEP 163
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RESULT 4
Q99XI2 PRELIMINARY; PRT; 280 AA.
ID Q99XI2;
AC Q99XI2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative ABC transporter (ATP-binding protein).
GN OrderedLocNames=SPY2194;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE006636; AAK34822.1; --
DR HSSP; Q58663; 1G9X.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Complete proteome.
KW SEQUENCE 280 AA; 30863 MW; DBE44F6F80C7D5 CRC64;
SQ

Query Match 7.9%; Score 22; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 FKKLHQSGMTIVLTHLMDVDA 209
DB 188 FKKLHQSGMTIVLTHLMDVDA 209

RESULT 5
Q7CWM8 PRELIMINARY; PRT; 280 AA.
ID Q7CWM8;
AC Q7CWM8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative ABC transporter (ATP-binding protein).
GN OrderedLocNames=spym18_2229;
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232;
RX MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
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RT Outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE010123; AAL98661.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 280 AA; 30663 MW; DBE44F6F8780C7D5 CRC64;

Query Match 7.9%; Score 22; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 FKXHQSGMTIVLTHLMDVVA 209
DB 188 FKXHQSGMTIVLTHLMDVVA 209

RESULT 6
QDRS0
ID QDRS0 PRELIMINARY; PRT; 280 AA.
AC QDRS0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative ABC transporter, ATP-binding protein; possible cobalt
DE transport system.
GN OrderedLocusNames=SMU.2149c;
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]_TaxID=1309;
RP SEQUENCE FROM N.A.
RC STRAIN=UAI59 / ATCC 700610 / Serotype c;
RX MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
RA Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
RA Qian Y., Li S., Zhu H., Najjar F.Z., Lai H., White J., Roe B.A.,
RA Ferratti J.J.;
RT "Genome sequence of Streptococcus mutans UAI59, a cariogenic dental
pathogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE015035; AAN59738.1; -.
DR HSP; P58301; IUS8.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 280 AA; 30941 MW; 600ED3F5C6F928A CRC64;

Query Match 7.9%; Score 22; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RT Outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE010123; AAL98661.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 280 AA; 30941 MW; 600ED3F5C6F928A CRC64;

Query Match 7.9%; Score 22; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RT Outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE010123; AAL98661.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 280 AA; 30941 MW; 600ED3F5C6F928A CRC64;

Query Match 7.9%; Score 22; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 PFELSGGQMRRAIAGILAMEP 164
DB 143 PFELSGGQMRRAIAGILAMEP 164

RESULT 7
QDRW4
ID QDRW4 PRELIMINARY; PRT; 280 AA.
AC QDRW4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 26, Last annotation update)
DE ABC transporter, ATP-binding protein.
GN OrderedLocusNames=SAG2150;
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]_TaxID=216466;
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=2222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
RA Tettein H., Maignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margalit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarcelli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE014289; AAN01008.1; -.
DR HSP; P58301; IUS8.
DR TIGR; SAG2150; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 280 AA; 31111 MW; 00253EF4A7E5C30B CRC64;

Query Match 7.9%; Score 22; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 PFELSGGQMRRAIAGILAMEP 164
DB 143 PFELSGGQMRRAIAGILAMEP 164

RESULT 8
QDE2L3
ID QDE2L3 PRELIMINARY; PRT; 280 AA.
AC QDE2L3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein gbs2109.
GN OrderedLocusNames=gbs2109;
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.

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OX NCBI_TaxID=216495;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MEM316 / Serotype III;
RA MEDLINE=2242508; PubMed=12354221;
RX Glaser P., Runiok C., Buchrieser C., Chevalier F., Frangeul L.,
RA Meadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease.";
RL Mol. Microbiol. 45:1499-1513 (2002).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL: AL766856; CAD47768.1; --
DR HSSP: P58301; IUSB.
DR Sagaliet; gbs2109; --
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR003593; AAA ATPase.
DR InterPro: IPR003439; ABC transporter.
DR Pfam: PF00005; ABC tran; 1.
DR ProDom: PD000006; ABC transporter; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE: PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 280 AA; 31111 MW; 00253EF4A7E5C30B CRC64;

Query Match 7.9%; Score 22; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 PFELSGGQRRVAIAGILAMEP 164
DB 143 PFELSGGQRRVAIAGILAMEP 164
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RESULT 9
Q8K5H2 PRELIMINARY; PRT; 280 AA.
ID Q8K5H2 Q79VY7;
AC Q8K5H2; Q79VY7;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Putative ABC transporter (ATP-binding protein).
GN OrderedLocusNames=SPB1841, SpvM3 1845;
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
RA Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Perkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SGI-1;
RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa I., Kurokawa K., Yanashita A., Nakata M., Tomiyasu Y.,
RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
RA Hayaishi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights

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RT into phage evolution.";
RL Genome Res. 13:1042-1055 (2003).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL: AE014172; AM80452.1; --
DR EMBL: AP005146; BAC64936.1; --
DR HSSP: Q58663; IG9X.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR003593; AAA ATPase.
DR InterPro: IPR003439; ABC transporter.
DR Pfam: PF00005; ABC tran; 1.
DR ProDom: PD000006; ABC transporter; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE: PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 280 AA; 30905 MW; 8E7752BD48834752 CRC64;

Query Match 7.9%; Score 22; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 FKLLHQSGMTIVLVTHLMDDDVA 209
DB 188 FKLLHQSGMTIVLVTHLMDDDVA 209
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RESULT 10
P70970 PRELIMINARY; PRT; 276 AA.
ID P70970 Q797S2;
AC P70970; Q797S2;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Hypothetical protein orf5 (YbaE protein).
GN Name=orf5; Synonyms=ybaE; OrderedLocusNames=BSU01460;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97124188; PubMed=8969501;
RA Yasumoto K., Liu H., Jeong S.M., Ohashi Y., Kakinuma S., Tanaka K.,
RA Kawamura F., Yoshikawa H., Takahashi H.;
RT "Sequence analysis of a 50 kb region between spoOH and rrnH on the
RT Bacillus subtilis chromosome.";
RL Microbiology 142:3039-3046 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriell S., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot P., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrati E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,

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RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivoita C., Rocha E., Roche B.,
RA Rose M., Sadale Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P.,
RA Shin B.S., Soldo B., Sorokin A., Taccioni E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassarotti A., Viari A., Wambuit R., Wedler E., Wedler H.,
RA Westzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
RA Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.",
RL Nature 390:249-256(1997).
CC -|- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; D64126; BAA10984.1; -.
DR EMBL; Z99104; CAB11922.1; -.
DR PIR; B69742; B69742.
DR HSSP; Q58663; 1G9X.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA-ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome; Hypothetical protein.
SQ SEQUENCE 276 AA; 30578 MW; ASAE1B64360016C9 CRC64;

Query Match 6.8%; Score 19; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 7.6e-10; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 DRSPFELSGGQMRRAIAG 158
DB 127 DRSPFELSGGQMRRAIAG 145

RESULT 11
Q65P76 PRELIMINARY; PRT; 289 AA.
AC Q65P76;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE YbaE (ABC transporter).
GN Name=YbaE; ORFNames=BL01022, BL100164;
OS Bacillus licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 13;
RX PubMed=15383718;
RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
RA Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R.,
RA Ehrenreich A., Gottschalk G.;
RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an
RT Organism with Great Industrial Potential.",
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14580;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,
RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
RA Berka R.M.;

RT "Complete genome sequence of the industrial bacterium Bacillus
RT licheniformis and comparisons with closely related Bacillus species.",
RL Genome Biol. 5:R77-R77(2004).
DR EMBL; AB017333; AAU39138.1; -.
DR EMBL; CP000002; AAU21793.1; -.
SQ SEQUENCE 289 AA; 32264 MW; 31B74C6C9B46A0AC CRC64;

Query Match 6.8%; Score 19; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 7.9e-10; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 DRSPFELSGGQMRRAIAG 158
DB 140 DRSPFELSGGQMRRAIAG 158

RESULT 12
Q8VNL8 PRELIMINARY; PRT; 177 AA.
AC Q8VNL8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative ABC transporter (Fragment).
OS Enterococcus faecium (Streptococcus faecium).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1352;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22105956; PubMed=12110480; DOI=10.1016/S0928-8244(02)00304-8;
RA Burnie J.P., Carter T.L., Rigg G.P., Hodgetts S.J., Donohoe M.S.,
RA Matthews R.C.;
RT "Identification of ABC transporters in vancomycin-resistant
RT Enterococcus faecium as potential targets for antibody therapy.",
CC -|- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AJ428868; CAD2181.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding.
FT NON TER 177
SQ SEQUENCE 177 AA; 19663 MW; B00F2778F106845F CRC64;

Query Match 6.5%; Score 18; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 5e-09; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 RSPFELSGGQMRRAIAG 158
DB 141 RSPFELSGGQMRRAIAG 158

RESULT 13
Q8V455 PRELIMINARY; PRT; 288 AA.
AC Q8V455;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Lmo2600 protein.
GN OrderedLocusNames=lmo2600;
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;

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RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordisiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AL591983; CAD00678.1; -.
DR PIR; AH1399; AH1399.
DR ListList; LMO2600; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0006166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
DR Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AL591983; CAD00678.1; -.
DR PIR; AH1399; AH1399.
DR ListList; LMO2600; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0006166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 288 AA; 31971 MW; 8628839C8CAEDBE0 CRC64;

Query Match 6.5%; Score 18; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 7.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 RSPFELSGGQMRRAIAG 158
DB 141 RSPFELSGGQMRRAIAG 158

RESULT 14
Q927N9 PRELIMINARY; PRT; 288 AA.
AC Q927N9;
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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordisiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AL591983; CAD00678.1; -.
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RA Peterson J.D., White O., Nelson M.C., Nierman W.C., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA Forberger H.A., Tran B., Kathariou S., Wonderling L.D., Uhlir G.A.,
RA Bayles D.O., Luchansky J.B., Fraser C.M.;
RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen Listeria monocytogenes reveal new insights into the core genome components of this species.";
RL Nucleic Acids Res. 32:2386-2395(2004).
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GenCore version 5.1.6
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(without alignments)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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138	8	2.9	407	16	US-10-425-115-33618	Sequence 33618, A	211	7	2.5	112	16	US-10-437-963-175313	Sequence 175313, A
139	8	2.9	433	18	US-10-501-282-6190	Sequence 6190, App	212	7	2.5	116	18	US-10-450-763-35261	Sequence 35261, A
140	8	2.9	467	15	US-10-424-599-161382	Sequence 161382, A	213	7	2.5	117	16	US-10-437-963-111007	Sequence 111007, A
141	8	2.9	475	14	US-10-076-157-4	Sequence 4, Appl	214	7	2.5	117	16	US-10-767-701-51081	Sequence 51081, A
142	8	2.9	479	15	US-10-369-493-17963	Sequence 17963, A	215	7	2.5	121	16	US-10-403-142-70	Sequence 70, Appl
143	8	2.9	483	16	US-10-425-115-333619	Sequence 333619, A	216	7	2.5	125	14	US-10-189-940-145	Sequence 145, App
144	8	2.9	506	15	US-10-282-122A-76906	Sequence 76906, A	217	7	2.5	125	16	US-10-403-142-66	Sequence 66, Appl
145	8	2.9	511	15	US-10-369-493-10376	Sequence 10376, A	218	7	2.5	125	15	US-10-971-479-145	Sequence 145, App
146	8	2.9	530	18	US-10-501-282-6192	Sequence 6192, App	219	7	2.5	127	15	US-10-094-749-2807	Sequence 2807, App
147	8	2.9	549	15	US-10-282-122A-50157	Sequence 50157, A	220	7	2.5	130	16	US-10-425-115-333951	Sequence 333951, A
148	8	2.9	555	18	US-08-781-986A-5247	Sequence 5247, App	221	7	2.5	131	16	US-10-767-701-33416	Sequence 33416, A
149	8	2.9	555	15	US-10-329-624-5247	Sequence 5247, App	222	7	2.5	133	16	US-10-437-963-112486	Sequence 112486, A
150	8	2.9	560	18	US-10-501-282-3004	Sequence 3004, App	223	7	2.5	133	16	US-10-425-115-274605	Sequence 274605, A
151	8	2.9	561	15	US-10-369-493-9808	Sequence 9808, App	224	7	2.5	142	9	US-09-966-546-22	Sequence 22, Appl
152	8	2.9	567	18	US-10-724-972A-7424	Sequence 7424, App	225	7	2.5	142	10	US-09-966-545-22	Sequence 22, Appl
153	8	2.9	572	18	US-10-501-282-6194	Sequence 6194, App	226	7	2.5	142	9	US-09-965-212-22	Sequence 22, Appl
154	8	2.9	574	18	US-10-501-282-6194	Sequence 6194, App	227	7	2.5	142	14	US-10-189-940-22	Sequence 22, Appl
155	8	2.9	575	15	US-10-369-493-18840	Sequence 18840, App	228	7	2.5	142	14	US-10-189-940-146	Sequence 146, App
156	8	2.9	576	15	US-10-369-493-19977	Sequence 19977, A	229	7	2.5	142	16	US-10-403-142-64	Sequence 64, Appl
157	8	2.9	583	9	US-09-815-242-13458	Sequence 13458, A	230	7	2.5	142	16	US-10-403-142-68	Sequence 68, Appl

231	7	2.5	142	18	US-10-971-479-22	Sequence 22, Appl	304	7	2.5	235	15	US-10-425-114-45258	Sequence 45258, A
232	7	2.5	142	18	US-10-971-479-146	Sequence 146, App	305	7	2.5	235	17	US-10-732-923-1558	Sequence 1558, Ap
233	7	2.5	143	17	US-10-732-923-24136	Sequence 24136, A	306	7	2.5	237	18	US-10-501-282-6270	Sequence 6270, Ap
234	7	2.5	143	17	US-10-732-923-24137	Sequence 24137, A	307	7	2.5	241	11	US-09-825-423C-6	Sequence 6, Appli
235	7	2.5	145	10	US-09-764-891-3645	Sequence 3645, Ap	308	7	2.5	241	11	US-10-425-114-42421	Sequence 42421, A
236	7	2.5	147	16	US-10-767-701-36763	Sequence 36763, A	309	7	2.5	244	15	US-10-424-599-171724	Sequence 171724, A
237	7	2.5	148	11	US-09-825-423C-3	Sequence 3, Appli	310	7	2.5	246	15	US-10-282-122A-49651	Sequence 49651, A
238	7	2.5	150	17	US-10-889-503-27	Sequence 27, Appl	311	7	2.5	247	15	US-10-156-761-13831	Sequence 13831, A
239	7	2.5	151	16	US-10-772-021-9	Sequence 9, Appli	312	7	2.5	248	14	US-09-738-626-6094	Sequence 6094, Ap
240	7	2.5	152	16	US-10-772-021-7	Sequence 7, Appli	313	7	2.5	249	9	US-10-501-282-6272	Sequence 6272, Ap
241	7	2.5	155	16	US-10-425-115-369032	Sequence 369032, A	314	7	2.5	251	18	US-10-501-282-6272	Sequence 119, App
242	7	2.5	157	13	US-10-071-751-18	Sequence 18, Appl	315	7	2.5	252	9	US-09-860-670-119	Sequence 119, App
243	7	2.5	157	13	US-09-921-397-84	Sequence 84, Appl	316	7	2.5	252	15	US-10-227-646-119	Sequence 45630, A
244	7	2.5	158	16	US-10-767-701-55394	Sequence 55394, A	317	7	2.5	256	16	US-10-767-701-45630	Sequence 301162, A
245	7	2.5	159	17	US-10-889-503-26	Sequence 26, Appl	318	7	2.5	256	16	US-10-425-115-301162	Sequence 301166, A
246	7	2.5	161	17	US-10-889-503-28	Sequence 28, Appl	319	7	2.5	256	16	US-10-425-115-301166	Sequence 1611, Ap
247	7	2.5	162	9	US-09-795-693-40	Sequence 40, Appl	320	7	2.5	257	20	US-11-097-143-1611	Sequence 18554, A
248	7	2.5	162	14	US-10-156-239-40	Sequence 40, Appl	321	7	2.5	258	15	US-10-369-493-18554	Sequence 5063, Ap
249	7	2.5	162	14	US-10-199-485-40	Sequence 40, Appl	322	7	2.5	260	15	US-10-369-493-5063	Sequence 11145, A
250	7	2.5	162	14	US-10-156-761-1786	Sequence 7786, Ap	323	7	2.5	262	14	US-10-156-761-11145	Sequence 85, Appl
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252	7	2.5	166	16	US-10-425-115-228496	Sequence 228496, A	325	7	2.5	263	17	US-10-391-939A-6	Sequence 32, Appl
253	7	2.5	173	16	US-10-767-701-61137	Sequence 61137, A	326	7	2.5	263	17	US-10-391-939A-32	Sequence 39, Appl
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256	7	2.5	176	15	US-10-472-928-1602	Sequence 1602, Ap	329	7	2.5	264	15	US-10-425-114-57651	Sequence 205747, A
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258	7	2.5	177	16	US-10-424-599-189639	Sequence 189639, A	331	7	2.5	266	20	US-11-126-662-7	Sequence 91, Appl
259	7	2.5	185	9	US-09-529-063-34	Sequence 34, Appl	332	7	2.5	267	15	US-10-461-194-91	Sequence 121, App
260	7	2.5	185	14	US-10-414-378-34	Sequence 34, Appl	333	7	2.5	267	15	US-10-461-194-121	Sequence 44154, A
261	7	2.5	189	15	US-10-369-493-9540	Sequence 9540, Ap	334	7	2.5	269	15	US-10-282-122A-44154	Sequence 71162, A
262	7	2.5	192	14	US-10-252-819-15	Sequence 15, Appl	335	7	2.5	269	17	US-10-282-122A-71162	Sequence 741, App
263	7	2.5	192	16	US-10-767-701-62326	Sequence 62326, A	336	7	2.5	272	10	US-09-884-456-84	Sequence 84, Appl
264	7	2.5	194	9	US-09-921-397-86	Sequence 86, Appl	337	7	2.5	272	10	US-09-884-456-84	Sequence 84, Appl
265	7	2.5	194	15	US-10-425-114-55787	Sequence 55787, A	338	7	2.5	272	15	US-10-424-599-177737	Sequence 177737, A
266	7	2.5	194	15	US-10-335-977-5407	Sequence 5407, Ap	339	7	2.5	274	9	US-09-815-242-5549	Sequence 5549, Ap
267	7	2.5	197	15	US-10-369-493-23120	Sequence 23120, A	340	7	2.5	274	15	US-10-282-122A-63496	Sequence 63496, A
268	7	2.5	197	15	US-10-627-476-470	Sequence 470, App	341	7	2.5	274	15	US-10-282-122A-64292	Sequence 64292, A
269	7	2.5	200	15	US-10-424-599-275210	Sequence 275210, A	342	7	2.5	275	14	US-10-156-761-12256	Sequence 12256, A
270	7	2.5	200	15	US-10-424-599-161479	Sequence 161479, A	343	7	2.5	275	17	US-10-732-923-1581	Sequence 1581, Ap
271	7	2.5	202	15	US-10-369-493-19395	Sequence 19395, A	344	7	2.5	276	17	US-10-732-923-1499	Sequence 1499, Ap
272	7	2.5	202	15	US-10-282-122A-48935	Sequence 48935, A	345	7	2.5	277	15	US-10-282-122A-53483	Sequence 53483, A
273	7	2.5	205	14	US-10-169-048-36	Sequence 36, Appl	346	7	2.5	277	15	US-10-651-165-278	Sequence 278, App
274	7	2.5	205	20	US-11-144-352-36	Sequence 36, Appl	347	7	2.5	277	15	US-10-651-165-277	Sequence 277, App
275	7	2.5	207	18	US-10-958-169-2	Sequence 2, Appli	348	7	2.5	278	9	US-09-921-397-83	Sequence 83, Appl
276	7	2.5	208	15	US-10-369-493-17420	Sequence 17420, A	349	7	2.5	278	15	US-10-282-122A-55379	Sequence 55379, A
277	7	2.5	209	18	US-10-721-922A-110	Sequence 110, App	350	7	2.5	278	15	US-10-651-165-57	Sequence 57, Appl
278	7	2.5	210	16	US-10-425-115-211307	Sequence 211307, A	351	7	2.5	278	15	US-10-651-165-178	Sequence 178, App
279	7	2.5	213	16	US-10-425-115-301161	Sequence 301161, A	352	7	2.5	278	15	US-10-651-165-265	Sequence 266, App
280	7	2.5	215	9	US-09-924-356A-36	Sequence 36, Appl	353	7	2.5	278	15	US-10-651-165-266	Sequence 267, App
281	7	2.5	215	16	US-10-437-963-166562	Sequence 166562, A	354	7	2.5	278	15	US-10-651-165-267	Sequence 268, App
282	7	2.5	215	16	US-10-425-115-251276	Sequence 251276, A	355	7	2.5	278	15	US-10-651-165-268	Sequence 269, App
283	7	2.5	216	16	US-10-425-115-239832	Sequence 239832, A	356	7	2.5	278	15	US-10-651-165-270	Sequence 270, App
284	7	2.5	216	17	US-10-732-923-5834	Sequence 5834, Ap	357	7	2.5	278	15	US-10-651-165-271	Sequence 271, App
285	7	2.5	219	16	US-10-767-701-52070	Sequence 52070, A	358	7	2.5	278	15	US-10-651-165-272	Sequence 272, App
286	7	2.5	220	15	US-10-369-493-9636	Sequence 9626, Ap	359	7	2.5	278	15	US-10-651-165-273	Sequence 273, App
287	7	2.5	221	15	US-10-282-122A-48012	Sequence 48012, A	360	7	2.5	278	15	US-10-651-165-274	Sequence 274, App
288	7	2.5	222	16	US-10-474-776-347	Sequence 347, App	361	7	2.5	278	15	US-10-651-165-275	Sequence 275, App
289	7	2.5	223	9	US-09-738-626-6926	Sequence 6926, Ap	362	7	2.5	278	15	US-10-651-165-276	Sequence 276, App
290	7	2.5	226	16	US-10-437-963-109136	Sequence 109136, A	363	7	2.5	278	16	US-10-703-086-2	Sequence 2, Appli
291	7	2.5	228	15	US-10-282-122A-65535	Sequence 65535, A	364	7	2.5	278	17	US-10-855-896-2	Sequence 52131, A
292	7	2.5	228	17	US-10-732-923-24129	Sequence 24129, A	365	7	2.5	279	15	US-10-282-122A-52131	Sequence 60654, A
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294	7	2.5	229	18	US-10-732-923-24131	Sequence 24131, A	367	7	2.5	279	18	US-10-450-763-56216	Sequence 346, App
295	7	2.5	230	15	US-10-369-493-172	Sequence 172, App	368	7	2.5	279	18	US-10-501-282-346	Sequence 4419, Ap
296	7	2.5	230	16	US-10-425-115-277148	Sequence 277148, A	369	7	2.5	280	18	US-10-724-972A-4419	Sequence 3124, Ap
297	7	2.5	232	15	US-10-369-493-7757	Sequence 7757, Ap	370	7	2.5	281	17	US-10-472-928-3124	Sequence 3, Appli
298	7	2.5	233	15	US-10-369-493-10533	Sequence 10533, A	371	7	2.5	282	14	US-10-188-012-3	Sequence 3, Appli
299	7	2.5	234	15	US-10-424-599-177736	Sequence 177736, A	372	7	2.5	282	17	US-10-863-497-3	Sequence 219, App
300	7	2.5	234	16	US-10-425-115-222781	Sequence 222781, A	373	7	2.5	284	15	US-10-289-762-219	Sequence 17, Appl
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302	7	2.5	235	15	US-10-282-122A-70031	Sequence 70031, A	375	7	2.5	285	14	US-10-242-568-17	Sequence 17, Appl
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377	7	2.5	285	15	US-10-282-122A-52539	Sequence 52539, A	450	7	2.5	311	9	US-09-808-589A-2	Sequence 2, Appli
378	7	2.5	288	11	US-09-825-423C-5	Sequence 5, Appli	451	7	2.5	311	9	US-09-553-874-4	Sequence 4, Appli
379	7	2.5	288	14	US-10-156-761-11595	Sequence 11595, A	452	7	2.5	311	10	US-09-808-898-18	Sequence 18, Appl
380	7	2.5	290	18	US-10-724-972A-6394	Sequence 6394, Ap	453	7	2.5	311	14	US-10-348-074-38	Sequence 38, Appl
381	7	2.5	291	15	US-10-369-493-19624	Sequence 19624, A	454	7	2.5	311	16	US-10-767-701-33503	Sequence 33503, A
382	7	2.5	292	15	US-10-424-599-148108	Sequence 148108, A	455	7	2.5	311	16	US-10-829-432-8	Sequence 8, Appli
383	7	2.5	292	17	US-10-732-923-1510	Sequence 1510, Ap	456	7	2.5	311	17	US-10-472-928-3580	Sequence 3580, Ap
384	7	2.5	293	9	US-09-738-626-4857	Sequence 4857, Ap	457	7	2.5	312	15	US-10-369-493-14590	Sequence 14590, A
385	7	2.5	294	15	US-10-414-219-2	Sequence 2, Appli	458	7	2.5	312	15	US-10-282-122A-77770	Sequence 77770, A
386	7	2.5	294	15	US-10-282-122A-76896	Sequence 76896, A	459	7	2.5	313	17	US-10-732-923-7802	Sequence 7802, Ap
387	7	2.5	295	10	US-09-896-032-2	Sequence 2, Appli	460	7	2.5	314	14	US-10-156-761-13748	Sequence 13748, A
388	7	2.5	295	15	US-10-425-114-45402	Sequence 45402, A	461	7	2.5	314	15	US-10-369-493-17049	Sequence 17049, A
389	7	2.5	295	17	US-10-802-891-2	Sequence 2, Appli	462	7	2.5	314	15	US-10-369-493-18123	Sequence 18123, A
390	7	2.5	296	16	US-10-425-115-363468	Sequence 363468, A	463	7	2.5	314	15	US-10-369-493-20982	Sequence 20982, A
391	7	2.5	297	15	US-10-369-493-9980	Sequence 9980, Ap	464	7	2.5	314	15	US-10-369-493-21632	Sequence 21632, A
392	7	2.5	297	15	US-10-369-493-11552	Sequence 11552, A	465	7	2.5	315	15	US-10-282-122A-60298	Sequence 60298, A
393	7	2.5	298	15	US-10-369-493-16121	Sequence 16121, A	466	7	2.5	315	15	US-10-282-122A-72901	Sequence 72901, A
394	7	2.5	298	15	US-10-369-493-20421	Sequence 20421, A	467	7	2.5	315	18	US-10-617-320-3914	Sequence 3914, Ap
395	7	2.5	298	15	US-10-282-122A-69688	Sequence 69688, A	468	7	2.5	316	15	US-10-369-493-18754	Sequence 18754, A
396	7	2.5	298	15	US-10-424-599-180038	Sequence 180038, A	469	7	2.5	316	15	US-10-369-493-20198	Sequence 20198, A
397	7	2.5	299	10	US-09-884-456-66	Sequence 66, Appl	470	7	2.5	317	15	US-10-282-122A-70784	Sequence 70784, A
398	7	2.5	299	10	US-09-884-456-68	Sequence 68, Appl	471	7	2.5	317	15	US-10-282-122A-71844	Sequence 71844, A
399	7	2.5	299	10	US-09-884-455-66	Sequence 66, Appl	472	7	2.5	319	15	US-10-724-972A-6323	Sequence 6323, Ap
400	7	2.5	299	15	US-09-884-455-68	Sequence 68, Appl	473	7	2.5	322	15	US-10-425-114-68400	Sequence 68400, A
401	7	2.5	299	15	US-10-369-493-13820	Sequence 13820, A	474	7	2.5	323	15	US-10-425-114-54322	Sequence 54322, A
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403	7	2.5	300	15	US-10-369-493-12609	Sequence 12609, A	476	7	2.5	326	15	US-10-282-122A-56065	Sequence 56065, A
404	7	2.5	300	15	US-10-369-493-17941	Sequence 17941, A	477	7	2.5	326	15	US-10-425-114-63180	Sequence 63180, A
405	7	2.5	300	16	US-10-703-086-5	Sequence 5, Appli	478	7	2.5	327	17	US-10-732-923-7822	Sequence 7822, Ap
406	7	2.5	300	17	US-10-855-897-1	Sequence 1, Appli	479	7	2.5	327	17	US-10-732-923-24135	Sequence 24135, A
407	7	2.5	300	17	US-10-855-896-1	Sequence 1, Appli	480	7	2.5	328	15	US-10-282-122A-42941	Sequence 42941, A
408	7	2.5	301	14	US-10-004-633-24	Sequence 24, Appl	481	7	2.5	328	16	US-10-425-115-341382	Sequence 341382, A
409	7	2.5	301	14	US-10-180-012-29	Sequence 29, Appl	482	7	2.5	330	15	US-10-407-920-36	Sequence 36, Appl
410	7	2.5	301	14	US-10-180-012-31	Sequence 31, Appl	483	7	2.5	330	15	US-10-425-114-58483	Sequence 58483, A
411	7	2.5	301	14	US-10-252-131-24	Sequence 24, Appl	484	7	2.5	330	15	US-10-425-115-318731	Sequence 318731, A
412	7	2.5	301	15	US-10-291-265-752	Sequence 752, App	485	7	2.5	331	14	US-10-156-761-13233	Sequence 13233, A
413	7	2.5	301	15	US-10-354-447-4	Sequence 4, Appli	486	7	2.5	333	15	US-10-282-122A-60539	Sequence 60539, A
414	7	2.5	301	15	US-10-354-447-6	Sequence 6, Appli	487	7	2.5	334	15	US-10-369-493-16769	Sequence 16769, A
415	7	2.5	301	15	US-10-264-237-2772	Sequence 2772, Ap	488	7	2.5	334	15	US-10-655-506-7	Sequence 7, Appli
416	7	2.5	301	17	US-10-663-497-29	Sequence 29, Appl	489	7	2.5	334	17	US-10-718-321-7	Sequence 7, Appli
417	7	2.5	301	17	US-10-663-497-31	Sequence 31, Appl	490	7	2.5	334	17	US-10-450-763-56327	Sequence 56327, A
418	7	2.5	301	17	US-10-838-852-24	Sequence 24, Appl	491	7	2.5	336	18	US-10-732-923-1569	Sequence 1569, Ap
419	7	2.5	301	18	US-10-958-169-13	Sequence 13, Appl	492	7	2.5	339	15	US-10-732-923-1771	Sequence 1771, Ap
420	7	2.5	302	10	US-09-896-032-9	Sequence 9, Appli	493	7	2.5	339	15	US-10-732-923-17857	Sequence 17857, A
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422	7	2.5	302	15	US-10-369-493-14945	Sequence 14945, A	495	7	2.5	339	9	US-09-808-589A-12	Sequence 12, Appl
423	7	2.5	302	17	US-10-802-891-9	Sequence 9, Appli	496	7	2.5	339	9	US-09-808-589A-14	Sequence 14, Appl
424	7	2.5	303	15	US-10-425-114-59721	Sequence 69721, A	497	7	2.5	339	9	US-09-808-589A-16	Sequence 16, Appl
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426	7	2.5	304	15	US-10-369-493-15736	Sequence 15736, A	499	7	2.5	339	17	US-10-391-939A-2	Sequence 2, Appli
427	7	2.5	304	15	US-10-369-493-20414	Sequence 20414, A	500	7	2.5	339	17	US-10-391-939A-28	Sequence 28, Appl
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429	7	2.5	305	17	US-10-663-497-1	Sequence 1, Appli	502	7	2.5	339	17	US-10-732-923-1569	Sequence 1569, Ap
430	7	2.5	306	9	US-09-815-243-12233	Sequence 12233, A	503	7	2.5	339	17	US-10-732-923-1771	Sequence 1771, Ap
431	7	2.5	306	15	US-10-369-493-9090	Sequence 9090, Ap	504	7	2.5	339	17	US-10-732-923-17857	Sequence 17857, A
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437	7	2.5	308	14	US-10-287-274-392	Sequence 392, App	510	7	2.5	339	17	US-10-732-923-24127	Sequence 24127, A
438	7	2.5	308	15	US-10-369-493-352	Sequence 352, App	511	7	2.5	340	9	US-09-738-626-5233	Sequence 5233, Ap
439	7	2.5	308	15	US-10-369-493-705	Sequence 705, App	512	7	2.5	340	17	US-10-732-923-17994	Sequence 17994, A
440	7	2.5	308	15	US-10-369-493-893	Sequence 893, App	513	7	2.5	341	15	US-10-282-122A-42782	Sequence 42782, A
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448	7	2.5	309	15	US-10-369-493-15520	Sequence 15520, A	521	7	2.5	343	17	US-10-472-928-3992	Sequence 3992, Ap
449	7	2.5	309	15	US-10-335-977-5408	Sequence 5408, Ap	522	7	2.5	344	14	US-10-173-480-20	Sequence 20, Appl

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530	7	2.5	346	14	US-10-156-761-14945	Sequence 14945, A	603	7	2.5	364	17	US-10-663-497-27	Sequence 27, Appl
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559	7	2.5	353	17	US-10-732-923-7806	Sequence 7806, Ap	632	7	2.5	383	16	US-10-468-356-136	Sequence 468, App
560	7	2.5	353	17	US-10-732-923-7818	Sequence 7818, Ap	633	7	2.5	384	16	US-10-767-701-45995	Sequence 45995, A
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562	7	2.5	353	17	US-10-732-923-7922	Sequence 7922, Ap	635	7	2.5	385	15	US-10-087-192-567	Sequence 567, App
563	7	2.5	353	17	US-10-732-923-7965	Sequence 7965, Ap	636	7	2.5	391	13	US-10-369-493-14363	Sequence 14363, A
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565	7	2.5	354	15	US-10-369-493-2800	Sequence 2800, Ap	638	7	2.5	394	16	US-10-767-701-45470	Sequence 45470, A
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574	7	2.5	356	17	US-10-732-923-7808	Sequence 7808, Ap	647	7	2.5	416	15	US-10-407-920-37	Sequence 37, Appl
575	7	2.5	357	17	US-10-732-923-7847	Sequence 7847, Ap	648	7	2.5	416	15	US-10-425-115-215475	Sequence 215475, A
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578	7	2.5	358	15	US-10-282-122A-77768	Sequence 77768, A	651	7	2.5	424	9	US-10-738-626-4359	Sequence 4359, Ap
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582	7	2.5	359	14	US-10-188-012-23	Sequence 23, Appl	655	7	2.5	424	16	US-10-732-923-785	Sequence 785, App
583	7	2.5	359	15	US-10-285-027-302	Sequence 302, App	656	7	2.5	424	17	US-10-732-923-816	Sequence 816, App
584	7	2.5	359	15	US-10-188-832-64	Sequence 64, Appl	657	7	2.5	424	17	US-10-369-493-3609	Sequence 3609, Ap
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591	7	2.5	359	17	US-10-847-918-25	Sequence 25, Appl	664	7	2.5	427	15	US-10-732-923-23956	Sequence 23956, A
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										452	17	US-10-774-721-18	Sequence 18, Appl
										452	17	US-10-732-923-11183	Sequence 11183, A
										454	17	US-10-732-923-8459	Sequence 8459, Ap

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671	7	2.5	461	16	US-10-425-115-263463	Sequence 263463, A	744	7	2.5	560	16	US-10-474-776-247	Sequence 247, App
672	7	2.5	465	14	US-10-232-643-2	Sequence 2, Appli	745	7	2.5	560	17	US-10-472-928-826	Sequence 826, App
673	7	2.5	467	15	US-10-424-599-230135	Sequence 230135, A	746	7	2.5	561	14	US-10-156-761-13374	Sequence 13374, A
674	7	2.5	470	16	US-10-425-115-327487	Sequence 327487, A	747	7	2.5	562	15	US-10-424-599-251264	Sequence 251264, A
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676	7	2.5	473	11	US-09-847-670-1	Sequence 1, Appli	749	7	2.5	564	15	US-10-282-122A-68510	Sequence 68510, A
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682	7	2.5	480	15	US-10-425-114-70221	Sequence 70221, A	755	7	2.5	575	17	US-10-473-193-54	Sequence 54, Appli
683	7	2.5	489	18	US-10-335-977-5328	Sequence 5328, App	756	7	2.5	576	15	US-10-424-599-173221	Sequence 173221, A
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685	7	2.5	490	15	US-10-369-493-21753	Sequence 21753, A	758	7	2.5	577	15	US-10-369-493-2917	Sequence 2917, App
686	7	2.5	490	16	US-10-425-115-305707	Sequence 305707, A	759	7	2.5	579	15	US-10-369-493-3014	Sequence 3014, App
687	7	2.5	491	18	US-10-840-060-186	Sequence 186, App	760	7	2.5	580	18	US-10-724-372A-7378	Sequence 7378, App
688	7	2.5	491	18	US-10-840-060-188	Sequence 188, App	761	7	2.5	581	15	US-10-369-493-454	Sequence 454, App
689	7	2.5	491	20	US-11-097-143-1713	Sequence 1713, App	762	7	2.5	581	15	US-10-369-493-9724	Sequence 9724, App
690	7	2.5	491	20	US-11-097-143-27966	Sequence 27966, A	763	7	2.5	581	15	US-10-369-493-19340	Sequence 19340, A
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698	7	2.5	504	17	US-10-952-045-6	Sequence 6, Appli	771	7	2.5	582	15	US-10-282-122A-73088	Sequence 73088, A
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ALIGNMENTS

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QY 61 QGSRVVPDTLITSTSKNKDIRQIRKQVGLVFPQFAENQIFETVLKDVAFQPNFGVSEED 120
DB 61 QGSRVVPDTLITSTSKNKDIRQIRKQVGLVFPQFAENQIFETVLKDVAFQPNFGVSEED 120
QY 121 AVKTAREKIALVGDIDSLFDRSPPELSCGQMRRAIAGILAMEPAIILVLDPTAGLDPLG 180
DB 121 AVKTAREKIALVGDIDSLFDRSPPELSCGQMRRAIAGILAMEPAIILVLDPTAGLDPLG 180
QY 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKPSDVFDQVVFME 240
DB 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKPSDVFDQVVFME 240
QY 241 EVQLGVPKITAFCRKLADRGVSKRLPIKIEEFKESLNG 279
DB 241 EVQLGVPKITAFCRKLADRGVSKRLPIKIEEFKESLNG 279
RESULT 2
US-10-472-928-4660
; Sequence 4660, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026926WO
; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4660
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; OTHER INFORMATION: ABC transporter, ATP-binding protein
; OTHER INFORMATION: Cellular location: membrane
; OTHER INFORMATION: Similar to strain R6 sequence 15904066 (e-154)
US-10-472-928-4660
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Query Match 100.0%; Score 279; DB 17; Length 279;
Best Local Similarity 100.0%; Pred. No. 2e-259;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIALENNVFTYQSGTPLASAAALSDVSLTIEDGSGYTALIGHTGSGKSTILQLLGLLVPS 60
DB 1 MGIALENNVFTYQSGTPLASAAALSDVSLTIEDGSGYTALIGHTGSGKSTILQLLGLLVPS 60
QY 61 QGSRVVPDTLITSTSKNKDIRQIRKQVGLVFPQFAENQIFETVLKDVAFQPNFGVSEED 120
DB 61 QGSRVVPDTLITSTSKNKDIRQIRKQVGLVFPQFAENQIFETVLKDVAFQPNFGVSEED 120
QY 121 AVKTAREKIALVGDIDSLFDRSPPELSCGQMRRAIAGILAMEPAIILVLDPTAGLDPLG 180
DB 121 AVKTAREKIALVGDIDSLFDRSPPELSCGQMRRAIAGILAMEPAIILVLDPTAGLDPLG 180
QY 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKPSDVFDQVVFME 240
DB 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKPSDVFDQVVFME 240
QY 241 EVQLGVPKITAFCRKLADRGVSKRLPIKIEEFKESLNG 279
DB 241 EVQLGVPKITAFCRKLADRGVSKRLPIKIEEFKESLNG 279
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US-10-617-320-4838

; Sequence 4838, Application US/10617320

; Publication No. US20050136404A1

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bueh

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID

SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE

FOR DIAGNOSTIC THERAPEUTICS

NUMBER OF SEQUENCES: 5206

CORRESPONDENCE ADDRESS:

ADDRESS: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: <unknown>

OPERATING SYSTEM: <unknown>

SOFTWARE: <unknown>

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/617,320

FILING DATE: 10-Jul-2003

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433

FILING DATE: 30-Jun-1998

APPLICATION NUMBER: 60/ 085131

FILING DATE: May 12, 1998

APPLICATION NUMBER: 60/051553

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 4838:

SEQUENCE CHARACTERISTICS:

LENGTH: 280 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...280

SEQUENCE DESCRIPTION: SEQ ID NO: 4838:

US-10-617-320-4838

RESULT 3	
US-10-617-320-4838	
; Sequence 4838, Application US/10617320	
; Publication No. US20050136404A1	
GENERAL INFORMATION:	
APPLICANT: Lynn A Doucette-Stamm and David Bueh	
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID	
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE	
FOR DIAGNOSTIC THERAPEUTICS	
NUMBER OF SEQUENCES: 5206	
CORRESPONDENCE ADDRESS:	
ADDRESS: GENOME THERAPEUTICS CORPORATION	
STREET: 100 Beaver Street	
CITY: Waltham	
STATE: Massachusetts	
COUNTRY: USA	
ZIP: 02354	
COMPUTER READABLE FORM:	
MEDIUM TYPE: CD-ROM ISO9660	
COMPUTER: <unknown>	
OPERATING SYSTEM: <unknown>	
SOFTWARE: <unknown>	
CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/10/617,320	
FILING DATE: 10-Jul-2003	
PRIOR APPLICATION DATA:	
APPLICATION NUMBER: US/09/107,433	
FILING DATE: 30-Jun-1998	
APPLICATION NUMBER: 60/ 085131	
FILING DATE: May 12, 1998	
APPLICATION NUMBER: 60/051553	
FILING DATE: July 2, 1997	
ATTORNEY/AGENT INFORMATION:	
NAME: Ariniello, Pamela Deneke	
REGISTRATION NUMBER: 40,489	
REFERENCE/DOCKET NUMBER: GTC-011	
TELECOMMUNICATION INFORMATION:	
TELEPHONE: (781)893-5007	
TELEFAX: (781)893-8277	
INFORMATION FOR SEQ ID NO: 4838:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 280 amino acids	
TYPE: amino acid	
TOPOLOGY: linear	
MOLECULE TYPE: protein	
HYPOTHETICAL: YES	
ORIGINAL SOURCE:	
ORGANISM: Streptococcus pneumoniae	
FEATURE:	
NAME/KEY: misc feature	
LOCATION: (B) LOCATION 1...280	
SEQUENCE DESCRIPTION: SEQ ID NO: 4838:	
US-10-617-320-4838	
Query Match	
Best Local Similarity 95.7%; Score 267; DB 18; Length 280;	
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MGTALENNVFTYQSGTPLASAAALSDVSLTTEDGSYTALIGHTGSGKSTILQLLNGLLVPS 60
Db	2 MGTALENNVFTYQSGTPLASAAALSDVSLTTEDGSYTALIGHTGSGKSTILQLLNGLLVPS 61
Qy	61 QGSVRVFDLTITSTKNKDIQIRKQVGLVFQFAENQIFETVLKDVAFGPQNFVSEED 120
Db	62 QGSVRVFDLTITSTKNKDIQIRKQVGLVFQFAENQIFETVLKDVAFGPQNFVSEED 121
Qy	121 AVKTAREKALVGVDESIFDRSPPELGGQMRRAIAGILAMEPAIILVLDPTAGLDPLG 180
Db	122 AVKTAREKALVGVDESIFDRSPPELGGQMRRAIAGILAMEPAIILVLDPTAGLDPLG 181
Qy	181 RKELMTLTKKLGHSQGMTIVLVTHLMDDAEYANQVYVMEKGRLVKGGKPSDFQDVVFME 240
US-09-815-242-13440	
; Sequence 13440, Application US/09815242	
; Patent No. US20020061569A1	
GENERAL INFORMATION:	
APPLICANT: Haselbeck, Robert	
APPLICANT: Ohlsen, Kari L.	
APPLICANT: Zyskind, Judith W.	
APPLICANT: Wall, Daniel	
APPLICANT: Trawick, John D.	
APPLICANT: Carr, Grant J.	
APPLICANT: Yamamoto, Robert T.	
APPLICANT: Xu, H. Howard	
TITLE OF INVENTION: Identification of Essential Genes in	
FILE OF INVENTION: Prokaryotes	
FILE REFERENCE: ELITRA.011A	
CURRENT APPLICATION NUMBER: US/09/815,242	
CURRENT FILING DATE: 2001-03-21	
PRIOR APPLICATION NUMBER: 60/191,078	
PRIOR FILING DATE: 2000-03-21	
PRIOR APPLICATION NUMBER: 60/206,848	
PRIOR FILING DATE: 2000-05-23	
PRIOR APPLICATION NUMBER: 60/207,727	
PRIOR FILING DATE: 2000-05-26	
PRIOR APPLICATION NUMBER: 60/242,578	
PRIOR FILING DATE: 2000-10-23	
PRIOR APPLICATION NUMBER: 60/253,625	
PRIOR FILING DATE: 2000-11-27	
PRIOR APPLICATION NUMBER: 60/257,931	
PRIOR FILING DATE: 2000-12-22	
PRIOR APPLICATION NUMBER: 60/269,308	
PRIOR FILING DATE: 2001-02-16	
NUMBER OF SEQ ID NOS: 14110	
SOFTWARE: FastSeq for Windows Version 4.0	
SEQ ID NO 13440	
LENGTH: 279	
TYPE: PRT	
ORGANISM: Streptococcus pneumoniae	
US-09-815-242-13440	
Query Match	
Best Local Similarity 59.9%; Score 167; DB 9; Length 279;	
Matches 267; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	12 YQSGTPLASAAALSDVSLTTEDGSYTALIGHTGSGKSTILQLLNGLLVPSQGSVRVFDTLI 71
Db	12 YQSGTPLASAAALSDVSLTTEDGSYTALIGHTGSGKSTILQLLNGLLVPSQGSVRVFDTLI 71
Qy	72 TSTSKNKDIQIRKQVGLVFQFAENQIFETVLKDVAFGPQNFVSEEDAVKTAREKAL 131
Db	72 TSTSKNKDIQIRKQVGLVFQFAENQIFETVLKDVAFGPQNFVSEEDAVKTAREKAL 131
Qy	132 VGIDESLFDSPPELGGQMRRAIAGILAMEPAIILVLDPTAGLDPLGRKELMTLTKKL 191
Db	132 VGIDESLFDSPPELGGQMRRAIAGILAMEPAIILVLDPTAGLDPLGRKELMTLTKKL 191
Qy	192 HQSGMTIVLVTHLMDDAEYANQVYVMEKGRLVKGGKPSDFQDVVFMEFVQLGVPKITA 251
Db	192 HQSGMTIVLVTHLMDDAEYANQVYVMEKGRLVKGGKPSDFQDVVFMEFVQLGVPKITA 251
Qy	252 FCRLADRGVSFKRLPIKIEEFKESLNG 279
Db	252 FCRLADRGVSFKRLPIKIEEFKESLNG 279
RESULT 5	


```

; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74821
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-282-122A-74821

Query Match          7.9%; Score 22; DB 15; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 FKXHQSGMTIVLVTHLMDVDA 209
DB 188 FKXHQSGMTIVLVTHLMDVDA 209

RESULT 8
US-10-369-493-23054
; Sequence 23054, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 23054
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-369-493-23054

Query Match          6.8%; Score 19; DB 15; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 140 DRSPFELSGGQMRRAIAG 158
DB 127 DRSPFELSGGQMRRAIAG 145

RESULT 9
US-10-054-968-2
; Sequence 2, Application US/10054968
; Publication No. US20030119101A1
; GENERAL INFORMATION:
; APPLICANT: NEUTEC PHARMA PLC
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF INFECTIONS OF GRAM
; TITLE OF INVENTION: POSITIVE
; TITLE OF INVENTION: COCCI
; FILE REFERENCE: PM 259204
; CURRENT APPLICATION NUMBER: US/10/054,968
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US/09/214,307
; PRIOR FILING DATE: 1999-01-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01830
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: GB9614274.0
; PRIOR FILING DATE: 1996-07-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-10-054-968-2

Query Match          6.5%; Score 18; DB 14; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 RSPFELSGGQMRRAIAG 158
DB 145 RSPFELSGGQMRRAIAG 162

RESULT 10
US-10-282-122A-45314
; Sequence 45314, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578

```

```
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45314
; TYPE: PRT
; ORGANISM: Bacillus anthracis
; NAME/KEY: MISC FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (24)..(24)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (39)..(39)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (43)..(43)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (124)..(124)
; OTHER INFORMATION: X=any amino acid
US-10-282-122A-45314
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```
Query Match          6.5%; Score 18; DB 15; Length 272;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 141 RSPFELSGQMRVAIAG 158
DB 133 RSPFELSGQMRVAIAG 150
```

```
RESULT 11
US-10-282-122A-60478
; Sequence 60478, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
```

```
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60478
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-10-282-122A-60478
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```
Query Match          6.5%; Score 18; DB 15; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 141 RSPFELSGQMRVAIAG 158
DB 141 RSPFELSGQMRVAIAG 158
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RESULT 12
US-10-282-122A-57659
; Sequence 57659, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
```

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; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57659
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-10-282-122A-57659

Query Match      6.5%; Score 18; DB 15; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 RSPFELSGGQMRVAIAG 158
Db 141 RSPFELSGGQMRVAIAG 158

RESULT 14
US-09-815-242-10545
; Sequence 10545, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10545
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10545

Query Match      6.1%; Score 17; DB 9; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 SPFELSGGQMRVAIAG 158
Db 142 SPFELSGGQMRVAIAG 158

RESULT 15
US-10-282-122A-57248
; Sequence 57248, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A

Query Match      6.5%; Score 18; DB 15; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 RSPFELSGGQMRVAIAG 158
Db 141 RSPFELSGGQMRVAIAG 158

RESULT 13
US-10-282-122A-46693
; Sequence 46693, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46693
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-282-122A-46693

Query Match      6.5%; Score 18; DB 15; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57248
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-282-122A-57248

Query Match      6.1%; Score 17; DB 15; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 142 SPFELSGGQMRVAIAG 158
Db 142 SPFELSGGQMRVAIAG 158
|||||
|||||

Search completed: October 28, 2005, 18:31:53
Job time : 188 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 17:07:43 ; Search time 170 Seconds
(without alignments)
634.742 Million cell updates/sec

Title: US-09-769-744D-26

Perfect score: 1387

Sequence: 1 MGIALENVNFYQEGTPLAS.....GVSPKRLPIKLEFPKESLNG 279

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq.16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1387	100.0	279	3 AAY81709	Streptococcus pneumoniae
2	1387	100.0	279	6 ABU2751	S. pneumoniae
3	1386	99.9	279	4 AAM01016	CFE 15 pr
4	1386	99.9	279	8 ADK47865	Streptococcus pneumoniae
5	1386	99.9	280	8 ADR96203	Novel S.
6	1378	99.4	279	4 AAU37847	Streptococcus pneumoniae
7	1378	99.4	279	6 ABU46314	Protein e
8	1002.5	72.3	280	5 ABU44574	Protein e
9	971	70.0	280	5 ABP26998	Streptococcus pneumoniae
10	971	70.0	280	5 ABP26997	Streptococcus pneumoniae
11	948	68.3	280	5 ABP26997	Streptococcus pneumoniae
12	948	68.3	280	8 ADK99875	Streptococcus pneumoniae
13	943	68.0	279	8 ADK99877	Streptococcus pneumoniae
14	943	68.0	279	8 ADK99878	Streptococcus pneumoniae
15	943	68.0	279	8 ADK99876	Streptococcus pneumoniae
16	943	68.0	279	8 ADK99883	Streptococcus pneumoniae
17	943	68.0	279	8 ADK99885	Streptococcus pneumoniae
18	943	68.0	279	8 ADK99879	Streptococcus pneumoniae
19	943	68.0	279	8 ADK99884	Streptococcus pneumoniae
20	940	67.8	279	8 ADK99880	Streptococcus pneumoniae
21	940	67.8	279	8 ADK99881	Streptococcus pneumoniae
22	940	67.8	279	8 ADK99882	Streptococcus pneumoniae
23	899.5	64.9	288	5 ABB53584	Lactococcus lactis
24	850.5	61.3	289	4 AAU34952	Enterococcus faecalis
25	850.5	61.3	289	6 ABU29324	Protein e

26	845.5	61.0	289	6 ABU29735	Protein e
27	844.5	60.9	316	7 ADH86847	Enterococcus faecalis
28	835.5	60.3	284	7 ADC96403	E. faeciu
29	794	57.2	292	6 ADB06402	Alloioococcus
30	794	57.2	294	6 ADB06404	Alloioococcus
31	729	52.6	276	8 ADS44624	Bacterial
32	700	50.5	293	6 ABU18769	Protein e
33	692.5	49.9	288	5 ABB47921	Listeria
34	692.5	49.9	288	6 ABU32554	Protein e
35	683	49.2	286	6 ABU24072	Protein e
36	661	47.7	288	6 ABU24767	Protein e
37	637.5	46.0	282	8 ADS28072	Bacterial
38	635.5	45.8	288	6 ABU25566	Protein e
39	611	44.1	286	6 ABU43237	Protein e
40	608	43.8	288	5 ABP38447	Staphylococcus aureus
41	608	43.8	288	8 ADS07134	Staphylococcus aureus
42	607	43.8	286	6 ABU43421	Protein e
43	594.5	42.9	286	4 AAU36641	Staphylococcus aureus
44	589.5	42.5	286	6 ABU16471	Protein e
45	589.5	42.5	286	6 ABM73355	Staphylococcus aureus

ALIGNMENTS

RESULT 1

AAV81709
ID AAY81709 standard; protein; 279 AA.

XX
AC AAY81709;

DT
XX 02-JUN-2000 (first entry)

DE Streptococcus pneumoniae protein sequence ID.

XX Streptococcus pneumoniae infection; immunogen; antigen; diagnosis; AIDS;
KW bacterial pneumonia; asplenia; heart disease; lung disease; alcoholism;
KW kidney disease; diabetes; immunosuppressive disorder; otitis media;
KW pneumococcal septicaemia; sinusitis; meningitis; therapy.

OS Streptococcus pneumoniae.

XX WO200006738-A2.

XX 10-FEB-2000.

PF 27-JUL-1999; 99WO-GB002452.

PR 27-JUL-1998; 98GB-00016336.

XX 19-MAR-1999; 99US-0125329P.

PA (MICR-) MICROBIAL TECHNIQS LTD.

PI Le Page RWF, Wells JM, Hanniffy SB, Hansbro PM;

XX WPI; 2000-195301/17.

DR N-PSDB; AA291805.

XX Streptococcal proteins and polynucleotides useful for diagnosis,

XX treatment and prophylaxis of bacterial infections.

PS Claim 2; Page 40; 76pp; English.

XX This sequence represents a Streptococcus pneumoniae protein of the
CC invention. The proteins (or their homologues, derivatives and/or
CC fragments) are useful as immunogens or antigens. Immunogenic or antigenic
CC compositions comprising the proteins are useful as vaccines and also in
CC diagnostic assays. The sequences are useful for the detection or
CC diagnosis of S. pneumoniae infection, by contacting a sample to be tested
CC with them. Agents capable of antagonising, inhibiting or interfering with
CC the function or expression of the protein or polypeptide are useful in
CC medical compositions in the treatment or prophylaxis of S. pneumoniae
CC infection. As the sequences can be used to treat S. pneumoniae infection,

CC they can be used to treat bacterial pneumonia, which has high rates in
CC young children, the elderly, and in patients with predisposing conditions
CC such as asplenia, heart, lung and kidney disease, diabetes, alcoholism,
CC or with immunosuppressive disorders, especially AIDS. They can also be
CC used to treat pneumococcal septicaemia, otitis media, sinusitis, and
CC meningitis
XX
SQ Sequence 279 AA;

Query Match 100.0%; Score 1387; DB 3; Length 279;
Best Local Similarity 100.0%; Pred. No. 5.8e-125;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGIALENVNTYQEGTGPLASAAALSDVSLTIEDGYSYALIGHTGSGKSTILOLLNGLLVPS 60
Db 1 MGIALENVNTYQEGTGPLASAAALSDVSLTIEDGYSYALIGHTGSGKSTILOLLNGLLVPS 60
Qy 61 QGSRVVPDTLITSTSKNDIRQIRKQVGLVQFAENQIFETVLKDVAFGQNFQVSEED 120
Db 61 QGSRVVPDTLITSTSKNDIRQIRKQVGLVQFAENQIFETVLKDVAFGQNFQVSEED 120
Qy 121 AVKTAREKALVGVIDESLFDSPPELGGQRRVAIAGILAMEPAAILVLDPTAGLDPLG 180
Db 121 AVKTAREKALVGVIDESLFDSPPELGGQRRVAIAGILAMEPAAILVLDPTAGLDPLG 180
Qy 181 RKELMTLPFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKPSDVFDQVWPE 240
Db 181 RKELMTLPFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKPSDVFDQVWPE 240
Qy 241 EVQLGVPKITAFCRKLADRGVSFKRLPIKIEFKESLNG 279
Db 241 EVQLGVPKITAFCRKLADRGVSFKRLPIKIEFKESLNG 279

RESULT 2
ID ABU02751 standard; protein; 279 AA.
XX
AC ABU02751;
XX
DT 23-OCT-2003 (revised)
DT 11-FEB-2003 (first entry)
XX
DE S. pneumoniae type 4 strain protein from coding region #2330.
XX
KW Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection;
KW antinflammatory; antibacterial; immunostimulant; auditory; respiratory;
KW gene therapy; vaccine.
XX
OS Streptococcus pneumoniae; type 4 strain.
XX
PN WO200277021-A2.
XX
PD 03-OCT-2002.
XX
PF 27-MAR-2002; 2002WO-IB002163.
XX
PR 27-MAR-2001; 2001GB-00007658.
XX
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX
PI Massignani V, Tettelin H, Fraser C;
XX
DR WPI; 2003-040579/03.
DR N-PSDB; ABX08042.
XX
PT New proteins and nucleic acid molecules from Streptococcus pneumoniae,
PT useful as medicaments for treating or preventing a disease or infection
PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
PT ear infection.
XX
PS Claim 1; SEQ ID NO 4660; 56pp; English.

XX
CC The invention relates to a protein comprising or having at least 50%
CC identity to any of the 2469 amino acid sequences, identified in the
CC specification (available on a computer readable format), or its fragment,
CC expressed from 2469 of 2489 identified DNA coding regions from the
CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as
CC ABS56454. Also included are an antibody which binds one of the proteins,
CC treating a patient by administering the protein, DNA or antibody (in a
CC composition), a kit comprising first and second primers, which are the
CC nucleic acid cited above or fragments between nucleotides 8-100 of a
CC sequence not defined in the specification, for amplifying a target
CC the first primer is substantially complementary to the target sequence, where
CC and the second primer is substantially complementary to the complement of
CC the target sequence, and where the parts of the primers having
CC substantial complementarity define the termini of the target sequence to
CC be amplified, assay comprising contacting a test compound with the
CC protein, and determining whether the test compound binds to the protein
CC and a Streptococcus pneumoniae bacterium, where one or more genes
CC encoding the proteins has been rendered inactive. The proteins, nucleic
CC acid molecules, antibody and compositions are useful as medicaments for
CC treating or preventing a disease or infection due to streptococcus
CC bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis
CC media or ear infection. They are also useful in developing vaccines,
CC diagnostics and antibiotics. The methods are useful for identifying
CC immunodominant proteins. The present sequence is one of the 2469 proteins
CC expressed by the identified coding regions from the genomic sequence.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 279 AA;

Query Match 100.0%; Score 1387; DB 6; Length 279;
Best Local Similarity 100.0%; Pred. No. 5.8e-125;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGIALENVNTYQEGTGPLASAAALSDVSLTIEDGYSYALIGHTGSGKSTILOLLNGLLVPS 60
Db 1 MGIALENVNTYQEGTGPLASAAALSDVSLTIEDGYSYALIGHTGSGKSTILOLLNGLLVPS 60
Qy 61 QGSRVVPDTLITSTSKNDIRQIRKQVGLVQFAENQIFETVLKDVAFGQNFQVSEED 120
Db 61 QGSRVVPDTLITSTSKNDIRQIRKQVGLVQFAENQIFETVLKDVAFGQNFQVSEED 120
Qy 121 AVKTAREKALVGVIDESLFDSPPELGGQRRVAIAGILAMEPAAILVLDPTAGLDPLG 180
Db 121 AVKTAREKALVGVIDESLFDSPPELGGQRRVAIAGILAMEPAAILVLDPTAGLDPLG 180
Qy 181 RKELMTLPFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKPSDVFDQVWPE 240
Db 181 RKELMTLPFKLHQSGMTIVLVTHLMDVVAEYANQVYVMEKGRLVKGGKPSDVFDQVWPE 240
Qy 241 EVQLGVPKITAFCRKLADRGVSFKRLPIKIEFKESLNG 279
Db 241 EVQLGVPKITAFCRKLADRGVSFKRLPIKIEFKESLNG 279

RESULT 3
ID AAM01016 standard; protein; 279 AA.
XX
AC AAM01016;
XX
DT 02-OCT-2001 (first entry)
XX
DE CFE 15 protein sequence.
XX
KW Antibacterial; vaccine; gene therapy; bacterial cell wall viability; CFE;
KW CEG; Conserved Essential Gene; bacterial infection; antisense therapy;
KW antibiotic resistance.
XX

OS	Streptococcus pneumoniae.	
XX		
PN	WO200149721-A2.	
XX		
XX	12-JUL-2001.	
XX		
PF	29-DEC-2000; 2000WO-US035604.	
XX		
XX	30-DEC-1999; 99US-0174089P.	
PR		
XX	(BRIM) BRISTOL-MYERS SQUIBB CO.	
PA		
XX	Dougherty TJ, Pucci MJ, Dougherty BA, Davison DB, Bruccoleri RE;	
PI	Thanassi JA;	
XX		
DR	WPI; 2001-496721/54.	
DR	N-PSDB; AAH90715.	
XX		
XX	Nucleic acids encoding conserved essential genes involved in bacterial	
PT	replication which are potential targets for the treatment of antibiotic	
PT	resistant bacterial infections.	
XX		
PS	Claim 27; Page 254-255; 380pp; English.	
XX		
CC	The present invention relates to nucleic acids (AAH90701-AAH90918)	
CC	encoding polypeptides (AAH01002-AAH0114), which are essential for the	
CC	viability of a bacterial cell wall. The acronym CFE stands for "CEG For	
CC	Expression", where CEG stands for "Conserved Essential Gene". The nucleic	
CC	acids are useful for detecting the presence of proteins essential for the	
CC	viability of a bacterial cell wall in samples such as cells, tissues,	
CC	biological fluids, blood, serum, nose, ear or throat swabs with ligands,	
CC	and for detecting corresponding target nucleic acid molecules with	
CC	complementary sequences. The nucleic acids are also useful for	
CC	determining whether a genomic nucleotide sequence of interest is	
CC	essential for viability of a bacterial cell or whether it resides within	
CC	an operon, by integrating an exogenous nucleotide sequence comprising a	
CC	portion of an open reading frame of the genomic sequence of interest	
CC	(comprising 200-500 base pairs) into the genomic sequence of interest	
CC	which confers a selectable phenotype to the cell, and determining cell	
CC	viability with a selection agent such as chloramphenicol. The nucleic	
CC	acids and proteins are also useful as vaccines and for treating bacterial	
CC	infections with gene therapy and antisense therapy. The nucleic acids	
CC	also enable identification of targets suitable for the treatment of	
CC	antibiotic resistant bacterial infections	
XX		
SQ	Sequence 279 AA;	
	Query Match 99.9%; Score 1386; DB 4; Length 279;	
	Best Local Similarity 99.6%; Pred. No. 7.2e-125;	
	Matches 278; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MGIALENVNFTYQEGTPLASAAALSDVSLTIEDGSGYTAGLIGTSGKSTILQLLGLLVPS 60	
Db	1 MGIALENVNFTYQEGTPLASAAALSDVSLTIEDGSGYTAGLIGTSGKSTILQLLGLLVPS 60	
Qy	61 QGSVRVPDITLTSTSKNKDIRQIRKQVGLVQFAENQIFETVLKDVAFQPGQFVSEED 120	
Db	61 QGSVRVPDITLTSTSKNKDIRQIRKQVGLVQFAENQIFETVLKDVAFQPGQFVSEED 120	
Qy	121 AVKTAREKALVGDIDSLFDRSPPELGGQRRVAIAGILAMEPAIILVLDDEPTAGLDPLG 180	
Db	121 AVKTAREKALVGDIDSLFDRSPPELGGQRRVAIAGILAMEPAIILVLDDEPTAGLDPLG 180	
Qy	181 RKELMTLTKKLHQSGMTIVLVTHLMDDDVAEYANQVYVMEKGRLVKGGKPSDVFQDVVME 240	
Db	181 RKELMTLTKKLHQSGMTIVLVTHLMDDDVAEYANQVYVMEKGRLVKGGKPSDVFQDVVME 240	
Qy	241 EVQLGVPKITAFACKRLADRGVSFKRLPIKIEEFKESLNG 279	
Db	241 EVQLGVPKITAFACKRLADRGVSFKRLPIKIEEFKESLNG 279	
	RESULT 4	

ADK47865	
ID	ADK47865 standard; protein; 279 AA.
XX	
AC	ADK47865;
XX	
DT	20-MAY-2004 (first entry)
XX	
DE	Streptococcus pneumoniae protein, Seq ID No 4380.
XX	
KW	Antibacterial; Gene therapy; Vaccine; Streptococcus pneumoniae.
XX	
OS	Streptococcus pneumoniae.
XX	
PN	US6699703-B1.
XX	
PD	02-MAR-2004.
XX	
PF	26-MAY-2000; 2000US-00583110.
XX	
PR	02-JUL-1997; 97US-0051553P.
PR	12-MAY-1998; 98US-0085131P.
PR	30-JUN-1998; 98US-00107433.
XX	
PA	(GENO-) GENOME THERAPEUTICS CORP.
XX	
PI	Doucette-Stamm L, Bush D, Zeng Q, Opperman T, Houseweart CE;
XX	
DR	WPI; 2004-212399/20.
DR	N-PSDB; ADK45204.
XX	
XX	New nucleic acid molecules and polypeptides useful for diagnosing,
PT	preventing and treating pathological conditions resulting from bacterial
PT	infection, e.g. Streptococcus pneumoniae infection, and in drug
PT	screening.
XX	
PS	Disclosure; SEQ ID NO 4380; 301pp; English.
XX	
CC	The invention relates to isolated Streptococcus pneumoniae nucleic acids
CC	and polypeptides. The nucleic acids and proteins are useful for
CC	diagnosing, preventing and treating pathological conditions resulting
CC	from bacterial infection, such as S. pneumoniae infection. These may also
CC	be used for drug screening procedures. The present sequence represents a
CC	Streptococcus pneumoniae polypeptide of the invention. Note: The sequence
CC	data for this patent did not appear in the printed specification but was
CC	obtained in electronic format directly from USPTO at
CC	seqdata.uspto.gov/sequence.html.
XX	
SQ	Sequence 279 AA;
	Query Match 99.9%; Score 1386; DB 8; Length 279;
	Best Local Similarity 99.6%; Pred. No. 7.2e-125;
	Matches 278; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MGIALENVNFTYQEGTPLASAAALSDVSLTIEDGSGYTAGLIGTSGKSTILQLLGLLVPS 60
Db	1 MGIALENVNFTYQEGTPLASAAALSDVSLTIEDGSGYTAGLIGTSGKSTILQLLGLLVPS 60
Qy	61 QGSVRVPDITLTSTSKNKDIRQIRKQVGLVQFAENQIFETVLKDVAFQPGQFVSEED 120
Db	61 QGSVRVPDITLTSTSKNKDIRQIRKQVGLVQFAENQIFETVLKDVAFQPGQFVSEED 120
Qy	121 AVKTAREKALVGDIDSLFDRSPPELGGQRRVAIAGILAMEPAIILVLDDEPTAGLDPLG 180
Db	121 AVKTAREKALVGDIDSLFDRSPPELGGQRRVAIAGILAMEPAIILVLDDEPTAGLDPLG 180
Qy	181 RKELMTLTKKLHQSGMTIVLVTHLMDDDVAEYANQVYVMEKGRLVKGGKPSDVFQDVVME 240
Db	181 RKELMTLTKKLHQSGMTIVLVTHLMDDDVAEYANQVYVMEKGRLVKGGKPSDVFQDVVME 240
Qy	241 EVQLGVPKITAFACKRLADRGVSFKRLPIKIEEFKESLNG 279
Db	241 EVQLGVPKITAFACKRLADRGVSFKRLPIKIEEFKESLNG 279

```

RESULT 5
ADR96203
ID ADR96203 standard; protein; 280 AA.
XX
AC ADR96203;
XX
DT 16-DEC-2004 (first entry)
XX
DE Novel S. pneumoniae protein sequence, SEQ ID 4838.
XX
KW Meningitis; bacteraemia; pneumonia; otitis media; vaccine;
KW bacterial infection.
XX
OS Streptococcus pneumoniae.
XX
PN US6800744-B1.
XX
PD 05-OCT-2004.
XX
PF 30-JUN-1998; 98US-00107433.
XX
PR 02-JUL-1997; 97US-0051553P.
XX
PR 12-MAY-1998; 98US-0085131P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Doucette-Stamm LA, Bush D;
XX
DR WPI, 2004-697205/68.
XX
DR N-PSDB; ADR93600.
XX
PT New isolated nucleic acid encoding a Streptococcus pneumoniae
PT polypeptide, useful for diagnosing, preventing and/or treating
PT pathological conditions resulting from the bacterial infection.
XX
PS Disclosure; SEQ ID NO 4838; 151pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising a sequence
CC encoding a Streptococcus pneumoniae ADR91366 polypeptide, or its
CC fragments, with any of 9 fully defined sequences (appearing as ADR94308,
CC ADR94489, ADR94800, ADR94837, ADR94969, ADR95253, ADR95642, ADR95682,
CC ADR96079) or any of the fully defined sequences appearing as ADR91705,
CC ADR91886, ADR92197, ADR92234, ADR93039, ADR93079, ADR92366, ADR92650 or
CC ADR93476 or at least 20 or 30 consecutive nucleotides of the nucleotide
CC sequences, or at least 40, 60 or 300 consecutive nucleotides, which is
CC hybridizable under high stringency conditions to the nucleotide sequence.
CC The nucleic acids and proteins are chosen from 5206 disclosed sequences.
CC Also included are a recombinant expression vector comprising the isolated
CC nucleic acid cited above operably linked to a transcription regulatory
CC element, a cell comprising the recombinant expression vector and a probe
CC comprising at least 20 consecutive nucleotides of the nucleotide
CC sequences as cited above. The methods and compositions of the present
CC invention are useful for the diagnosis, prevention and/or treatment of
CC pathological conditions resulting from bacterial infection by
CC Streptococcus pneumoniae e.g. pneumonia, bacteraemia, meningitis and
CC otitis media. The present sequence is one of the 2603 disclosed S.
CC pneumoniae protein sequences. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=6800744B1.
XX
SQ Sequence 280 AA;
Query Match 99.9%; Score 1386; DB 8; Length 280;
Best Local Similarity 99.6%; Pred No. 7.3e-125;
Matches 278; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIALENVFTYQEGTPLASALSVDLSLTIEDGYSYALIGHTGSGKSTILQNLGLVPS 60
DB 2 MGIALENVFTYQEGTPLASALSVDLSLTIEDGYSYALIGHTGSGKSTILQNLGLVPS 61
QY 61 QGSVRVFDTLITSTSKNKDIRQIRKQVGLVQFAENQIFBETVLKDVAFGPNFGVSEED 120

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Db 62 QGSVRVFDTLITSTSKNKDIRQIRKQVGLVQFAENQIFBETVLKDVAFGPNFGVSEED 121
QY 121 AVKTAREKALVIGIDESLFDSPFELSGGQMRRAIAGILAMEPAIILVLDPTAGLDPLG 180
Db 122 AVKTAREKALVIGIDESLFDSPFELSGGQMRRAIAGILAMEPAIILVLDPTAGLDPLG 181
QY 181 RKELMTLTKKLGSGMTIVLVTHLMDVAVYANQVYVMEKGRVKGKPSDFQDVVPM 240
Db 182 RKELMTLTKKLGSGMTIVLVTHLMDVAVYANQVYVMEKGRVKGKPSDFQDVVPM 241
QY 241 EVQLGVPKITAFCKRLADRGVSPKRLPIKIEEPKESLNG 279
Db 242 EVQLGVPKITAFCKRLADRGVSPKRLPIKIEEPKESLNG 280

RESULT 6
AAU37847
ID AAU37847 standard; protein; 279 AA.
XX
AC AAU37847;
XX
DT 14-FEB-2002 (first entry)
XX
DE Streptococcus pneumoniae cellular proliferation protein #276.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
XX
OS Streptococcus pneumoniae.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
XX
PR 23-MAY-2000; 2000US-0206848P.
XX
PR 26-MAY-2000; 2000US-0207727P.
XX
PR 23-OCT-2000; 2000US-0242578P.
XX
PR 27-NOV-2000; 2000US-0253625P.
XX
PR 22-DEC-2000; 2000US-0257931P.
XX
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
WPI; 2001-611495/70.
XX
DR N-PSDB; AAS55706.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
Example 3; SEQ ID NO 13440; 511pp; English.
XX
The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the genes,
XX their use in the discovery of novel antibiotics, the essential genes
XX themselves and the encoded proteins. The prokaryotes used are Escherichia
XX coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX useful for the identification of potential new targets for antibiotic
XX development. The antisense nucleic acids can also be used to identify
XX proteins used in proliferation, to express these proteins, and to obtain
XX antibodies capable of binding to the expressed proteins. The proteins can
XX be used to screen compounds in rational drug discovery programmes. The
XX antisense nucleic acid sequence is also useful to screen for homologous
XX nucleic acids which are required for cell proliferation in a wide variety
XX of organisms. The present sequence represents an essential prokaryotic
XX cellular proliferation protein. Note: The sequence data for this patent

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CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 279 AA;

Query Match 99.4%; Score 1378; DB 4; Length 279;
 Best Local Similarity 99.3%; Pred. No. 4.3e-124;
 Matches 277; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGIALENNVFTYQEGTFLASAAALSDVSLTIEDGSYTALIGHTGSGKSTILQINGLLVPS 60
 DB 1 MGIALENNVFTYQEGTFLASAAALSDVSLTIEDGSYTALIGHTGSGKSTILQINGLLVPS 60
 QY 61 QGSRVDFDLTSTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFQPNFGVSEED 120
 DB 61 QGSRVDFDLTSTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFQPNFGVSEED 120
 QY 121 AVKTAREKALVGDIDSLDFRSPFELSGGOMRVAIAGILAMEPAILVLDEPTAGLDPLG 180
 DB 121 AVKTAREKALVGDIDSLDFRSPFELSGGOMRVAIAGILAMEPAILVLDEPTAGLDPLG 180
 QY 181 RKELMTLFLKHLHSGMTIVLVTHLMDDDVAEYANQVYVMEKGRVLKGGKPSDVFQVVFME 240
 DB 181 RKELMTLFLKHLHSGMTIVLVTHLMDDDVAEYANQVYVMEKGRVLKGGKPSDVFQVVFME 240
 QY 241 EVOLGVPKITAFCKRLADRGVSFKRLPIKIEEPKESLING 279
 DB 241 EVOLGVPKITAFCKRLADRGVSFKRLPIKIEEPKESLING 279

RESULT 7
 ABU46314
 ID ABU46314 standard; protein; 279 AA.
 XX
 AC ABU46314;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #31841.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX Streptococcus pneumoniae.
 XX WO200277183-A2.
 PD 03-OCT-2002.
 XX 21-MAR-2002; 2002WO-US009107.
 XX 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (BLIT-) ELITRA PHARM INC.
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlson KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACA50184.
 XX
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 XX Claim 25; SEQ ID NO 74238; 1766pp; English.
 XX
 XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression

of the nucleic acid inhibits proliferation of a cell. Also included are:
 (1) a vector comprising a promoter operably linked to the nucleic acid
 encoding a polypeptide whose expression is inhibited by the antisense
 nucleic acid; (2) a host cell containing the vector; (3) an isolated
 polypeptide or its fragment whose expression is inhibited by the
 antisense nucleic acid; (4) an antibody capable of specifically binding
 the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 proliferation or the activity of a gene in an operon required for
 proliferation; (7) identifying a compound that influences the activity of
 the gene product or that has an activity against a biological pathway
 required for proliferation, or that inhibits cellular proliferation; (8)
 identifying a gene required for cellular proliferation or the biological
 pathway in which a proliferation-required gene or its gene product lies
 or a gene on which the test compound that inhibits proliferation of an
 organism acts; (9) manufacturing an antibiotic; (10) profiling a
 compound's activity; (11) a culture comprising strains in which the gene
 product is overexpressed or underexpressed; (12) determining the extent
 to which each of the strains is present in a culture or collection of
 strains; or (13) identifying the target of a compound that inhibits the
 proliferation of an organism. The antisense nucleic acids are useful for
 identifying proteins or screening for homologous nucleic acids required
 for cellular proliferation to isolate candidate molecules for rational
 drug discovery programs, or for screening homologous nucleic acids
 required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
K. pneumoniae or *P. aeruginosa*. The present sequence is encoded by one of
 the target prokaryotic essential genes. Note: The sequence data for this
 patent did not form part of the printed specification, but was obtained
 in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 279 AA;

Query Match 99.4%; Score 1378; DB 6; Length 279;
 Best Local Similarity 99.3%; Pred. No. 4.3e-124;
 Matches 277; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGIALENNVFTYQEGTFLASAAALSDVSLTIEDGSYTALIGHTGSGKSTILQINGLLVPS 60
 DB 1 MGIALENNVFTYQEGTFLASAAALSDVSLTIEDGSYTALIGHTGSGKSTILQINGLLVPS 60
 QY 61 QGSRVDFDLTSTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFQPNFGVSEED 120
 DB 61 QGSRVDFDLTSTSKNKDIQIRKQVGLVFOFAENQIFETVLKDVAFQPNFGVSEED 120
 QY 121 AVKTAREKALVGDIDSLDFRSPFELSGGOMRVAIAGILAMEPAILVLDEPTAGLDPLG 180
 DB 121 AVKTAREKALVGDIDSLDFRSPFELSGGOMRVAIAGILAMEPAILVLDEPTAGLDPLG 180
 QY 181 RKELMTLFLKHLHSGMTIVLVTHLMDDDVAEYANQVYVMEKGRVLKGGKPSDVFQVVFME 240
 DB 181 RKELMTLFLKHLHSGMTIVLVTHLMDDDVAEYANQVYVMEKGRVLKGGKPSDVFQVVFME 240
 QY 241 EVOLGVPKITAFCKRLADRGVSFKRLPIKIEEPKESLING 279
 DB 241 EVOLGVPKITAFCKRLADRGVSFKRLPIKIEEPKESLING 279

RESULT 8
 ABU44574
 ID ABU44574 standard; protein; 280 AA.
 XX
 AC ABU44574;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #30101.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX Streptococcus mutans.
 XX WO200277183-A2.
 PN
 XX

Matches 191; Conservative 35; Mismatches 51; Indels 0; Gaps 0;

QY 1 MGIALENNFTVQEGTPLASALSDVSLTIEDGSYTALIGHTSGKSTILOLLGLVPS 60
DB 1 MSINLQNVSYTYQAGTFPEGRALFNILNLDGSYTAFIGHTSGKSTIMQLLGLHVPT 60

QY 61 QGSVRVFDLTITSTSKNDIROIKQVGLVFOFAENQIFETVLKDVAFGPQNGVSEED 120
DB 61 TGIVSVDDKQDITNHSKNKEIKSRKHVGLVFPFESQLFEETVLKDVAFGPQNGVSP 120

QY 121 AVKTAREKALVIGIDESLDFRSPFELSGGQMRVAIAGILAMEPAILVLDDEPTAGLDPLG 180
DB 121 AEALAREKALVIGISENLFKNPFELSGGQMRVAIAGILAMQPKVLVLDDEPTAGLDPKG 180

QY 181 RKELMTLTKLHQSGMTIVLVTHLMDDDVAEYANQVVMKGLVKGKSDVQDVVEME 240
DB 181 RKELMTIFKKLHQSGMTIVLVTHLMDDDVANYADVVLDKGIILSGKPKTIFQQVSLLE 240

QY 241 EVOLGVPKITAFCCKLADRGVSFKRLPIKIEEPKESL 277
DB 241 KKQLGVPKVTUKLAQRVLDKGIPISSLPITLELREVL 277

RESULT 10

ABU46897

ID ABU46897 standard; protein; 280 AA.

XX

AC ABU46897;

DT 19-JUN-2003 (first entry)

XX

DE Protein encoded by Prokaryotic essential gene #32424.

XX

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX

OS Streptococcus pyogenes.

XX

XX WO200277183-A2.

XX

PD 03-OCT-2002.

XX

PF 21-MAR-2002; 2002WO-US009107.

XX

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX

PA (BLIT-) ELITRA PHARM INC.

Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

WPI; 2003-029926/02.

DR N-PSDB; ACA50767.

XX

XX New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

XX

PS Claim 25; SEQ ID NO 74821; 1766pp; English.

XX

XX The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 280 AA;

Query Match 70.0%; Score 971; DB 6; Length 280;

Best Local Similarity 69.0%; Pred. No. 7e-85;

Matches 191; Conservative 35; Mismatches 51; Indels 0; Gaps 0;

QY 1 MGIALENNFTVQEGTPLASALSDVSLTIEDGSYTALIGHTSGKSTILOLLGLVPS 60
DB 1 MSINLQNVSYTYQAGTFPEGRALFNILNLDGSYTAFIGHTSGKSTIMQLLGLHVPT 60

QY 61 QGSVRVFDLTITSTSKNDIROIKQVGLVFOFAENQIFETVLKDVAFGPQNGVSEED 120
DB 61 TGIVSVDDKQDITNHSKNKEIKSRKHVGLVFPFESQLFEETVLKDVAFGPQNGVSP 120

QY 121 AVKTAREKALVIGIDESLDFRSPFELSGGQMRVAIAGILAMEPAILVLDDEPTAGLDPLG 180
DB 121 AEALAREKALVIGISENLFKNPFELSGGQMRVAIAGILAMQPKVLVLDDEPTAGLDPKG 180

QY 181 RKELMTLTKLHQSGMTIVLVTHLMDDDVAEYANQVVMKGLVKGKSDVQDVVEME 240
DB 181 RKELMTIFKKLHQSGMTIVLVTHLMDDDVANYADVVLDKGIILSGKPKTIFQQVSLLE 240

QY 241 EVOLGVPKITAFCCKLADRGVSFKRLPIKIEEPKESL 277
DB 241 KKQLGVPKVTUKLAQRVLDKGIPISSLPITLELREVL 277

RESULT 11

ABP26997

ID ABP26997 standard; protein; 280 AA.

XX

AC ABP26997;

DT 02-JUL-2002 (first entry)

XX

DE Streptococcus polypeptide SEQ ID NO 3170.

XX

XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.

XX

OS Streptococcus agalactiae.

XX

PN WO200234771-A2.

XX

PD 02-MAY-2002.

XX

XX 29-OCT-2001; 2001WO-GB004789.

PF 27-OCT-2000; 2000GB-00026333.

PR 24-NOV-2000; 2000GB-00028727.

PR 07-MAR-2001; 2001GB-00005640.
XX (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX Telford J, Massignani V, Margarit Y Rosi, Grandi G, Fraser C;
PI Tettelin H;
XX WPI; 2002-352536/38.
DR N-P9DB; ABN67628.
XX New Streptococcus protein for the treatment or prevention of infection or
PT disease caused by Streptococcus bacteria, such as meningitis, and for
PT detecting a compound that binds to the protein.
XX Claim 1; Page 3470; 4525pp; English.
PS
XX The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and anti-inflammatory
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins
XX
SQ Sequence 280 AA;
Query Match 68.3%; Score 948; DB 5; Length 280;
Best Local Similarity 66.8%; Pred. No. 1.2e-82;
Matches 185; Conservative 39; Mismatches 53; Indels 0; Gaps 0;
QY 1 MGIALENVFTYQEGTPLASALSVDLSLTIEDGSYTALIGHTSGKSTILQNLGLLVP 60
DB 1 MGIEPKNVSYTYQAGTPPEGRALFDVNLKIEDASYTAFIGHTSGKSTIMQLLGLHIPT 60
QY 61 QGSVRFDTLITSTSKNDIRQIRKQVGLVFOFAENQIFETVLKDVAFGPQNFVSEED 120
DB 61 KGEVIVDDFSIKAGDKNKEIFIRKQVGLVFPFESQLFEETVLKDVAFGPQNFVSEED 120
QY 121 AVKTAREKALVIGIDESLFDSPFELSGGQMRRAIAGILAMEPAAILVLDPTAGLDPLG 180
DB 121 AERLAEEKLRLVIGISEDLDKPNPFELSGGQMRRAIAGILAMEPAAILVLDPTAGLDPLG 180
QY 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVAVYANQVYVMEKRLVKGKPSDFQDVVME 240
DB 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVAVYANQVYVMEKRLVKGKPSDFQDVVME 240
QY 241 EVQLGVPKITAFCKRLADRGVSKRLPIKIEFKESL 277
DB 241 SKQLGVPKITKPAQLSHKGLNPLSLPITINEFVEAI 277
RESULT 12
ADK99875
ID ADK99875 standard; protein; 280 AA.
XX ADK99875;
AC ADK99875;
XX 20-MAY-2004 (first entry)
DT Streptococcus agalactiae ORF SAG2150-related protein 1.
DE Streptococcus agalactiae ORF SAG2150-related protein 1.
XX immunogenic composition; group B Streptococcus; GBS; antibacterial;

streptococcal infection; vaccine; SAG.
XX Streptococcus agalactiae 2603V/R.
XX WO2004018646-A2.
XX 04-MAR-2004.
XX 26-AUG-2003; 2003WO-US026827.
XX 26-AUG-2002; 2002US-0406237P.
PR 27-AUG-2002; 2002US-0406676P.
PR 28-AUG-2002; 2002US-0406757P.
XX (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX Tettelin H, Massignani V;
XX WPI; 2004-248071/23.
XX Immunogenic composition useful as a vaccine for treating or preventing
PT streptococcal infections, comprises group B Streptococcus polypeptides.
PT Claim 10; SEQ ID NO 7912; 1194pp; English.
PS
XX The invention relates to a novel immunogenic composition comprising a
CC combination of 2-5 group B Streptococcus (GBS) polypeptides. Each
CC polypeptide is encoded by a GBS polynucleotide sequence which is
CC homologous to a polynucleotide sequence of group A Streptococcus (GAS),
CC Streptococcus pneumoniae and/or at least one other GBS serotype. The
CC composition of the invention demonstrates antibacterial activity whilst
CC the polypeptides and polynucleotides may be useful in assays to diagnose
CC and identify streptococcal infections or for identifying, screening and
CC developing vaccines and other treatments for streptococcal infections.
CC The current sequence is that of a Streptococcus agalactiae ORF SAG
CC protein of the invention.
XX
SQ Sequence 280 AA;
Query Match 68.3%; Score 948; DB 8; Length 280;
Best Local Similarity 66.8%; Pred. No. 1.2e-82;
Matches 185; Conservative 39; Mismatches 53; Indels 0; Gaps 0;
QY 1 MGIALENVFTYQEGTPLASALSVDLSLTIEDGSYTALIGHTSGKSTILQNLGLLVP 60
DB 1 MGIEPKNVSYTYQAGTPPEGRALFDVNLKIEDASYTAFIGHTSGKSTIMQLLGLHIPT 60
QY 61 QGSVRFDTLITSTSKNDIRQIRKQVGLVFOFAENQIFETVLKDVAFGPQNFVSEED 120
DB 61 KGEVIVDDFSIKAGDKNKEIFIRKQVGLVFPFESQLFEETVLKDVAFGPQNFVSEED 120
QY 121 AVKTAREKALVIGIDESLFDSPFELSGGQMRRAIAGILAMEPAAILVLDPTAGLDPLG 180
DB 121 AERLAEEKLRLVIGISEDLDKPNPFELSGGQMRRAIAGILAMEPAAILVLDPTAGLDPLG 180
QY 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVAVYANQVYVMEKRLVKGKPSDFQDVVME 240
DB 181 RKELMTLFPKLLHQSGMTIVLVTHLMDVAVYANQVYVMEKRLVKGKPSDFQDVVME 240
QY 241 EVQLGVPKITAFCKRLADRGVSKRLPIKIEFKESL 277
DB 241 SKQLGVPKITKPAQLSHKGLNPLSLPITINEFVEAI 277
RESULT 13
ADK99877
ID ADK99877 standard; protein; 279 AA.
XX ADK99877;
AC ADK99877;
XX 20-MAY-2004 (first entry)
DT Streptococcus agalactiae ORF SAG2150-related protein 1.
DE Streptococcus agalactiae ORF SAG2150-related protein 1.
XX immunogenic composition; group B Streptococcus; GBS; antibacterial;

```
DE Streptococcus agalactiae ORF SAG2150-related protein 3.
XX immunogenic composition; group B Streptococcus; GBS; antibacterial;
KW streptococcal infection; vaccine; SAG.
OS Streptococcus agalactiae.
XX WO2004018646-A2.
XX 04-MAR-2004.
PD 26-AUG-2003; 2003WO-US026827.
PF 26-AUG-2002; 2002US-0406237P.
PR 27-AUG-2002; 2002US-040676P.
PR 28-AUG-2002; 2002US-0406757P.
XX (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX Tettelin H, Massignani V;
XX WPI; 2004-248071/23.
DR Immunogenic composition useful as a vaccine for treating or preventing
XX streptococcal infections, comprises group B Streptococcus polypeptides.
XX Claim 10; SEQ ID NO 7914; 1194pp; English.
XX The invention relates to a novel immunogenic composition comprising a
XX combination of 2-5 group B Streptococcus (GBS) polypeptides. Each
XX polypeptide is encoded by a GBS polynucleotide sequence which is
XX homologous to a polynucleotide sequence of group A Streptococcus (GAS),
XX Streptococcus pneumoniae and/or at least one other GBS serotype. The
XX composition of the invention demonstrates antibacterial activity whilst
XX the polypeptides and polynucleotides may be useful in assays to diagnose
XX and identify streptococcal infections or for identifying, screening and
XX developing vaccines and other treatments for streptococcal infections.
XX The current sequence is that of a Streptococcus agalactiae ORF SAG
XX protein of the invention.
XX Sequence 279 AA;
Query Match 68.0%; Score 943; DB 8; Length 279;
Best Local Similarity 66.7%; Pred. No. 3.5e-82;
Matches 184; Conservative 39; Mismatches 53; Indels 0; Gaps 0;
QY 2 GIALENNVFTYQGTPLASAAALSDVSLTIEDGYSYTAIIGHGTSGKSTILQLLGLLVPSQ 61
DB 1 GIEFKNVSYTYQAGTFEGRALFDVNLKIEDASYTAFIGHTSGKSTIMQLLGLHIPTK 60
QY 62 GSVRVFDTLITSTSKNDIRQIRKQVGLVFQPAENQIFETVLKDVAFQPNFGVSEDA 121
DB 61 GEIVVDVDFSIKAGDKNKEIKFIRKQVGLVFQFPESQLFEETVLKDVAFQPNFGISQIEA 120
QY 122 VKTAREKALVGDIESLFRSPPELSCGQRRVAIAGILAMEPAIILVDEPTAGLDPLGR 181
DB 121 ERLAEKRLVIGSIEDLFDKNPELSCGQRRVAIAGILAMEPKVLVDEPTAGLDPKGR 180
QY 182 KELMTLPKLLHOSGMTIVLVTHLMDVDAEVANOVYVMEKRLVKGGKPSDVFDVVFME 241
DB 181 KELMTLPKLLHOSGMTIVLVTHLMDVDAEVANOVYVMEKRLVKGGKPSDVFDVVFME 240
QY 242 VOLGVPKITAFCKRLADRGVSFKRLPIKIEEFKESL 277
DB 241 KQLGVPKITKFAQLSHKGLNPLSLPITINEFVEAI 276
RESULT 14
ADK99878
ID ADK99878 standard; protein; 279 AA.
XX AC ADK99878;
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XX 20-MAY-2004 (first entry)
XX Streptococcus agalactiae ORF SAG2150-related protein 4.
DE immunogenic composition; group B Streptococcus; GBS; antibacterial;
KW streptococcal infection; vaccine; SAG.
OS Streptococcus agalactiae.
XX WO2004018646-A2.
XX 04-MAR-2004.
PD 26-AUG-2003; 2003WO-US026827.
PF 26-AUG-2002; 2002US-0406237P.
PR 27-AUG-2002; 2002US-040676P.
PR 28-AUG-2002; 2002US-0406757P.
XX (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX Tettelin H, Massignani V;
XX WPI; 2004-248071/23.
DR Immunogenic composition useful as a vaccine for treating or preventing
XX streptococcal infections, comprises group B Streptococcus polypeptides.
XX Claim 10; SEQ ID NO 7915; 1194pp; English.
XX The invention relates to a novel immunogenic composition comprising a
XX combination of 2-5 group B Streptococcus (GBS) polypeptides. Each
XX polypeptide is encoded by a GBS polynucleotide sequence which is
XX homologous to a polynucleotide sequence of group A Streptococcus (GAS),
XX Streptococcus pneumoniae and/or at least one other GBS serotype. The
XX composition of the invention demonstrates antibacterial activity whilst
XX the polypeptides and polynucleotides may be useful in assays to diagnose
XX and identify streptococcal infections or for identifying, screening and
XX developing vaccines and other treatments for streptococcal infections.
XX The current sequence is that of a Streptococcus agalactiae ORF SAG
XX protein of the invention.
XX Sequence 279 AA;
Query Match 68.0%; Score 943; DB 8; Length 279;
Best Local Similarity 66.7%; Pred. No. 3.5e-82;
Matches 184; Conservative 39; Mismatches 53; Indels 0; Gaps 0;
QY 2 GIALENNVFTYQGTPLASAAALSDVSLTIEDGYSYTAIIGHGTSGKSTILQLLGLLVPSQ 61
DB 1 GIEFKNVSYTYQAGTFEGRALFDVNLKIEDASYTAFIGHTSGKSTIMQLLGLHIPTK 60
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QY 122 VKTAREKALVGDIESLFRSPPELSCGQRRVAIAGILAMEPAIILVDEPTAGLDPLGR 181
DB 121 ERLAEKRLVIGSIEDLFDKNPELSCGQRRVAIAGILAMEPKVLVDEPTAGLDPKGR 180
QY 182 KELMTLPKLLHOSGMTIVLVTHLMDVDAEVANOVYVMEKRLVKGGKPSDVFDVVFME 241
DB 181 KELMTLPKLLHOSGMTIVLVTHLMDVDAEVANOVYVMEKRLVKGGKPSDVFDVVFME 240
QY 242 VOLGVPKITAFCKRLADRGVSFKRLPIKIEEFKESL 277
DB 241 KQLGVPKITKFAQLSHKGLNPLSLPITINEFVEAI 276
RESULT 15
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OM protein - protein search, using sw model

Run on: October 28, 2005, 18:04:45 ; Search time 43 Seconds
(without alignments)
484.351 Million cell updates/sec

Title: US-09-769-744D-26

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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10	10	3.6	292	4	US-09-602-787A-352
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103	7	2.5	272	1	US-08-709-173-84	Sequence 84, Appl	176	7	2.5	310	4	US-09-614-912-202	Sequence 202, Appl
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114	7	2.5	278	4	US-08-635-886C-267	Sequence 267, App	187	7	2.5	316	4	US-09-543-681A-6184	Sequence 6184, Ap
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122	7	2.5	278	4	US-08-635-886C-275	Sequence 275, App	195	7	2.5	334	4	US-09-197-970B-7	Sequence 7, Appl
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144	7	2.5	290	3	US-09-134-001C-3273	Sequence 14260, A	217	7	2.5	364	4	US-10-173-480-32	Sequence 32, Appl
145	7	2.5	290	4	US-09-902-540-16248	Sequence 3273, Ap	218	7	2.5	367	4	US-10-173-480-38	Sequence 38, Appl
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252	7	2.5	548	4	US-09-107-532A-6627	Sequence 6627, Ap	325	7	2.5	687	1	US-08-188-281B-14	Sequence 14, Appl
253	7	2.5	554	4	US-09-614-912-200	Sequence 200, App	326	7	2.5	687	5	PCT-US94-07280-14	Sequence 14, Appl
254	7	2.5	554	4	US-09-614-912-200	Sequence 200, App	327	7	2.5	687	5	PCT-US95-01087-14	Sequence 3, Appl
255	7	2.5	569	4	US-09-902-540-16735	Sequence 16735, A	328	7	2.5	694	3	US-08-895-522-3	Sequence 3, Appl
256	7	2.5	575	4	US-09-134-000C-5386	Sequence 5386, Ap	329	7	2.5	694	3	US-09-195-391-3	Sequence 3, Appl
257	7	2.5	580	3	US-09-134-001C-5611	Sequence 5611, Ap	330	7	2.5	715	4	US-09-543-681A-4943	Sequence 4943, Ap
258	7	2.5	582	4	US-09-489-039A-12080	Sequence 12080, A	331	7	2.5	728	4	US-09-881-239-1	Sequence 1, Appl
259	7	2.5	590	3	US-08-850-328-3	Sequence 3, Appl	332	7	2.5	739	3	US-08-444-818-148	Sequence 148, App
260	7	2.5	593	4	US-09-543-681A-5368	Sequence 5368, Ap	333	7	2.5	747	3	US-08-895-522-1	Sequence 1, Appl
261	7	2.5	594	4	US-09-107-532A-7250	Sequence 7250, Ap	334	7	2.5	747	3	US-09-195-391-1	Sequence 1, Appl
262	7	2.5	609	1	US-08-324-377-40	Sequence 40, Appl	335	7	2.5	780	4	US-09-603-208A-146	Sequence 146, App
263	7	2.5	609	2	US-08-384-616-40	Sequence 40, Appl	336	7	2.5	781	3	US-08-867-611-4	Sequence 4, Appl
264	7	2.5	609	3	US-09-904-686A-40	Sequence 40, Appl	337	7	2.5	781	4	US-09-690-359-4	Sequence 9, Appl
265	7	2.5	613	4	US-09-315-850-40	Sequence 40, Appl	338	7	2.5	781	5	PCT-US92-06965A-9	Sequence 64, Appl
266	7	2.5	623	4	US-10-104-966-6	Sequence 6, Appl	339	7	2.5	798	1	US-08-190-802A-64	Sequence 68, Appl
267	7	2.5	623	4	US-09-252-991A-31173	Sequence 31173, A	340	7	2.5	798	1	US-08-190-802A-68	Sequence 2, Appl
268	7	2.5	628	4	US-09-360-545-4	Sequence 4, Appl	341	7	2.5	798	2	US-08-308-818-2	Sequence 2, Appl
269	7	2.5	628	4	US-09-398-395A-20	Sequence 20, Appl	342	7	2.5	798	3	US-08-477-346-64	Sequence 64, Appl
270	7	2.5	628	4	US-09-887-586A-20	Sequence 20, Appl	343	7	2.5	798	3	US-08-477-346-68	Sequence 68, Appl
271	7	2.5	628	4	US-09-895-752-20	Sequence 20, Appl	344	7	2.5	798	3	US-08-473-089-64	Sequence 64, Appl
272	7	2.5	628	4	US-09-903-012B-20	Sequence 20, Appl	345	7	2.5	798	3	US-08-473-089-68	Sequence 64, Appl
273	7	2.5	631	1	US-09-900-797-20	Sequence 20, Appl	346	7	2.5	798	4	US-08-487-072A-64	Sequence 68, Appl
274	7	2.5	631	2	US-08-700-356-1	Sequence 1, Appl	347	7	2.5	798	4	US-08-487-072A-68	Sequence 68, Appl
275	7	2.5	631	2	US-08-936-865-1	Sequence 1, Appl	348	7	2.5	829	4	US-08-444-818-69	Sequence 59, Appl
276	7	2.5	631	2	US-08-833-678A-1	Sequence 1, Appl	349	7	2.5	829	4	US-09-881-239-5	Sequence 86, Appl
277	7	2.5	631	3	US-09-128-314-2	Sequence 2, Appl	350	7	2.5	841	1	US-08-350-884-86	Sequence 86, Appl
278	7	2.5	631	3	US-08-529-169A-1	Sequence 1, Appl	351	7	2.5	841	1	US-08-709-173-86	Sequence 86, Appl
279	7	2.5	631	3	US-08-483-799-1	Sequence 1, Appl	352	7	2.5	841	2	US-08-709-177-86	Sequence 52, Appl
280	7	2.5	632	3	US-09-198-723A-23	Sequence 23, Appl	353	7	2.5	971	3	US-08-867-611-52	Sequence 52, Appl
281	7	2.5	632	4	US-09-684-881-23	Sequence 23, Appl	354	7	2.5	971	3	US-09-690-359-53	Sequence 53, Appl
282	7	2.5	633	4	US-09-583-110-3803	Sequence 3803, Ap	355	7	2.5	973	3	US-09-690-359-53	Sequence 53, Appl
283	7	2.5	638	3	US-09-288-391-25	Sequence 25, Appl	356	7	2.5	973	4	US-09-252-991A-18616	Sequence 54, Appl
284	7	2.5	646	3	US-09-198-723A-60	Sequence 60, Appl	357	7	2.5	981	3	US-08-667-611-54	Sequence 54, Appl
285	7	2.5	646	3	US-09-198-723A-63	Sequence 63, Appl	358	7	2.5	992	4	US-09-690-359-54	Sequence 54, Appl
286	7	2.5	646	3	US-09-198-723A-66	Sequence 66, Appl	359	7	2.5	992	4	US-09-690-359-54	Sequence 54, Appl
287	7	2.5	646	3	US-09-198-723A-72	Sequence 69, Appl	360	7	2.5	1021	1	US-07-910-760-12	Sequence 12, Appl
288	7	2.5	646	3	US-09-684-881-60	Sequence 60, Appl	361	7	2.5	1021	1	US-08-440-519-12	Sequence 12, Appl
289	7	2.5	646	4	US-09-684-881-63	Sequence 63, Appl	362	7	2.5	1021	3	US-08-440-549-12	Sequence 12, Appl
290	7	2.5	646	4	US-09-684-881-66	Sequence 66, Appl	363	7	2.5	1099	4	US-09-881-654-4	Sequence 4, Appl
291	7	2.5	646	4	US-09-684-881-69	Sequence 69, Appl	364	7	2.5	1099	4	US-09-881-654-4	Sequence 4, Appl
292	7	2.5	646	4	US-09-684-881-72	Sequence 72, Appl	365	7	2.5	1147	1	US-10-637-323-4	Sequence 38, Appl
293	7	2.5	650	4	US-09-107-433-3849	Sequence 3849, Ap	366	7	2.5	1147	2	US-08-131-365B-38	Sequence 38, Appl
294	7	2.5	660	4	US-09-583-110-4478	Sequence 4478, Ap	367	7	2.5	1164	4	US-08-668-123-38	Sequence 38, Appl
295	7	2.5	664	4	US-09-107-433-3490	Sequence 3490, Ap	368	7	2.5	1196	4	US-09-949-016-9845	Sequence 9845, Ap
296	7	2.5	665	4	US-09-543-376B-1	Sequence 1, Appl	369	7	2.5	1272	4	US-09-949-016-7472	Sequence 19876, A
297	7	2.5	665	4	US-09-543-376B-2	Sequence 2, Appl	370	7	2.5	1307	1	US-08-395-246C-2	Sequence 7472, Ap
298	7	2.5	665	4	US-09-543-376B-3	Sequence 3, Appl	371	7	2.5	1308	2	US-08-936-644-2	Sequence 2, Appl
299	7	2.5	666	3	US-09-198-723A-11	Sequence 11, Appl	372	7	2.5	1308	3	US-09-352-552-2	Sequence 2, Appl
300	7	2.5	666	3	US-09-198-723A-12	Sequence 12, Appl	373	7	2.5	1375	3	US-08-665-259-26	Sequence 26, Appl
301	7	2.5	666	3	US-09-198-723A-13	Sequence 13, Appl	374	7	2.5	1375	3	US-08-762-500-26	Sequence 26, Appl
302	7	2.5	666	3	US-09-198-723A-14	Sequence 14, Appl	375	7	2.5	1422	4	US-08-469-260A-83	Sequence 83, Appl
303	7	2.5	666	3	US-09-198-723A-15	Sequence 15, Appl	376	7	2.5	1422	4	US-08-488-446-83	Sequence 83, Appl
304	7	2.5	666	3	US-09-198-723A-16	Sequence 16, Appl	377	7	2.5	1422	4	US-08-467-344A-83	Sequence 83, Appl
305	7	2.5	666	3	US-09-198-723A-17	Sequence 17, Appl	378	7	2.5	1457	3	US-08-424-550B-83	Sequence 83, Appl
306	7	2.5	666	3	US-09-198-723A-18	Sequence 18, Appl	379	7	2.5	1457	3	US-08-665-259-27	Sequence 27, Appl
307	7	2.5	666	4	US-09-684-881-11	Sequence 11, Appl	380	7	2.5	1457	3	US-08-762-500-27	Sequence 27, Appl
308	7	2.5	666	4	US-09-684-881-12	Sequence 12, Appl	381	7	2.5	1472	4	US-09-032-438C-119	Sequence 119, App
309	7	2.5	666	4	US-09-684-881-13	Sequence 13, Appl	382	7	2.5	1475	2	US-09-256-703-2	Sequence 2, Appl
310	7	2.5	666	4	US-09-684-881-14	Sequence 14, Appl	383	7	2.5	1479	2	US-08-951-912-4	Sequence 4, Appl
311	7	2.5	666	4	US-09-684-881-15	Sequence 15, Appl	384	7	2.5	1479	3	US-09-174-077-4	Sequence 4, Appl
312	7	2.5	666	4	US-09-684-881-16	Sequence 16, Appl	385	7	2.5	1480	1	US-07-637-621-2	Sequence 2, Appl
313	7	2.5	666	4	US-09-684-881-17	Sequence 17, Appl	386	7	2.5	1480	1	US-08-136-742A-2	Sequence 2, Appl
314	7	2.5	666	4	US-09-684-881-18	Sequence 18, Appl	387	7	2.5	1480	1	US-08-135-809A-2	Sequence 2, Appl
315	7	2.5	672	3	US-09-198-723A-19	Sequence 19, Appl	388	7	2.5	1480	1	US-08-466-886-17	Sequence 17, Appl
316	7	2.5	672	3	US-09-198-723A-20	Sequence 20, Appl	389	7	2.5	1480	2	US-08-951-912-2	Sequence 2, Appl
317	7	2.5	672	4	US-09-684-881-19	Sequence 19, Appl	390	7	2.5	1480	2	US-08-951-912-6	Sequence 6, Appl
318	7	2.5	672	4	US-09-684-881-20	Sequence 20, Appl	391	7	2.5	1480	2	US-08-469-461-2	Sequence 2, Appl
319	7	2.5	686	1	US-08-350-884-70	Sequence 70, Appl	392	7	2.5	1480	2	US-08-469-461-4	Sequence 4, Appl

393	7	2.5	1480	2	US-08-691-605-2	Sequence 2, Appli	466	7	2.5	2307	4	US-10-191-966-16	Sequence 16, Appli
394	7	2.5	1480	2	US-08-455-552A-14	Sequence 14, Appli	467	7	2.5	2436	3	US-08-444-818-75	Sequence 75, Appli
395	7	2.5	1480	3	US-07-890-609-2	Sequence 2, Appli	468	7	2.5	2560	1	US-09-949-016-11554	Sequence 11554, A
396	7	2.5	1480	3	US-07-890-609-4	Sequence 4, Appli	469	7	2.5	2620	4	US-08-324-977-32	Sequence 32, Appli
397	7	2.5	1480	3	US-09-248-026-2	Sequence 2, Appli	470	7	2.5	2620	2	US-08-384-616-32	Sequence 32, Appli
398	7	2.5	1480	3	US-08-469-617-17	Sequence 17, Appli	471	7	2.5	2620	2	US-08-904-686A-32	Sequence 32, Appli
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401	7	2.5	1480	3	US-09-174-077-2	Sequence 2, Appli	474	7	2.5	2621	2	US-08-384-616-36	Sequence 36, Appli
402	7	2.5	1480	3	US-09-174-077-6	Sequence 6, Appli	475	7	2.5	2621	2	US-08-904-686A-36	Sequence 36, Appli
403	7	2.5	1480	4	US-09-425-453A-2	Sequence 2, Appli	476	7	2.5	2621	3	US-09-315-850-36	Sequence 36, Appli
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408	7	2.5	1480	4	US-09-425-453A-12	Sequence 12, Appli	481	7	2.5	2864	4	US-08-424-550B-394	Sequence 394, Appli
409	7	2.5	1480	4	US-09-425-453A-14	Sequence 14, Appli	482	7	2.5	2894	2	US-08-466-975A-23	Sequence 23, Appli
410	7	2.5	1480	4	US-09-425-453A-16	Sequence 16, Appli	483	7	2.5	2894	2	US-08-391-671A-23	Sequence 23, Appli
411	7	2.5	1480	4	US-09-425-453A-18	Sequence 18, Appli	484	7	2.5	2894	3	US-08-467-902A-23	Sequence 23, Appli
412	7	2.5	1480	4	US-09-425-453A-20	Sequence 20, Appli	485	7	2.5	2894	3	US-09-275-265-23	Sequence 23, Appli
413	7	2.5	1480	4	US-08-469-630-17	Sequence 17, Appli	486	7	2.5	2894	4	US-09-941-611-23	Sequence 23, Appli
414	7	2.5	1480	4	US-09-949-016-5949	Sequence 5949, Ap	487	7	2.5	2955	2	US-08-443-260-3	Sequence 3, Appli
415	7	2.5	1480	5	PCT-US93-11667-2	Sequence 2, Appli	488	7	2.5	2955	3	US-08-442-805A-3	Sequence 3, Appli
416	7	2.5	1480	5	Patent No. 5240846	Sequence 2, Appli	489	7	2.5	2955	3	US-08-443-900A-3	Sequence 3, Appli
417	7	2.5	1480	6	Patent No. 5240846	Sequence 2, Appli	490	7	2.5	2955	3	US-08-444-818-124	Sequence 124, Appli
418	7	2.5	1480	6	Sequence 11311, A	Sequence 11311, A	491	7	2.5	2955	3	US-08-249-843-3	Sequence 3, Appli
419	7	2.5	1501	4	US-09-949-016-11311	Sequence 7, Appli	492	7	2.5	2955	3	US-08-444-818-138	Sequence 138, Appli
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421	7	2.5	1548	2	US-08-460-907B-7	Sequence 7, Appli	494	7	2.5	3010	1	US-08-324-977-14	Sequence 14, Appli
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423	7	2.5	1648	5	PCT-US94-07280-12	Sequence 12, Appli	496	7	2.5	3010	2	US-08-384-616-14	Sequence 14, Appli
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426	7	2.5	1692	3	US-09-263-933-11	Sequence 11, Appli	499	7	2.5	3010	3	US-09-014-416-3	Sequence 3, Appli
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441	7	2.5	2013	2	US-08-384-616-12	Sequence 12, Appli	514	7	2.5	3011	2	US-08-440-210-36	Sequence 36, Appli
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443	7	2.5	2013	3	US-09-315-850-12	Sequence 12, Appli	516	7	2.5	3011	2	US-08-710-637-2	Sequence 2, Appli
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446	7	2.5	2201	4	US-09-539-601-6	Sequence 6, Appli	519	7	2.5	3011	3	US-08-444-818-177	Sequence 177, App
447	7	2.5	2201	4	US-09-539-601-15	Sequence 15, Appli	520	7	2.5	3011	3	US-09-014-416-1	Sequence 1, Appli
448	7	2.5	2201	4	US-10-029-907-3	Sequence 3, Appli	521	7	2.5	3011	3	US-09-014-416-5	Sequence 5, Appli
449	7	2.5	2261	3	US-08-444-818-66	Sequence 66, Appli	522	7	2.5	3011	3	US-08-529-169A-6	Sequence 6, Appli
450	7	2.5	2261	4	US-09-526-193A-1	Sequence 1, Appli	523	7	2.5	3011	3	US-09-388-874-2	Sequence 2, Appli
451	7	2.5	2261	4	US-09-032-438C-118	Sequence 118, App	524	7	2.5	3011	3	US-09-046-604-36	Sequence 36, Appli
452	7	2.5	2261	4	US-09-596-141C-2	Sequence 2, Appli	525	7	2.5	3011	3	US-08-440-549-10	Sequence 10, Appli
453	7	2.5	2261	4	US-09-596-141C-8	Sequence 8, Appli	526	7	2.5	3011	3	US-08-850-328-1	Sequence 1, Appli
454	7	2.5	2261	4	US-09-596-141C-10	Sequence 10, Appli	527	7	2.5	3011	3	US-09-034-756-20	Sequence 20, Appli
455	7	2.5	2261	4	US-09-595-526C-2	Sequence 2, Appli	528	7	2.5	3011	4	US-09-483-799-6	Sequence 6, Appli
456	7	2.5	2261	4	US-09-595-526C-8	Sequence 8, Appli	529	7	2.5	3011	4	US-09-916-359-2	Sequence 2, Appli
457	7	2.5	2261	4	US-09-595-526C-10	Sequence 10, Appli	530	7	2.5	3011	4	US-10-104-966-1	Sequence 1, Appli
458	7	2.5	2307	3	US-08-263-933-2	Sequence 2, Appli	531	7	2.5	3011	4	US-09-952-572-9	Sequence 9, Appli
459	7	2.5	2307	3	US-08-263-933-9	Sequence 9, Appli	532	7	2.5	3011	5	PCT-US91-02225-10	Sequence 10, Appli
460	7	2.5	2307	3	US-09-263-933-16	Sequence 16, Appli	533	7	2.5	3011	5	PCT-US93-00907-1	Sequence 1, Appli
461	7	2.5	2307	4	US-09-919-901-2	Sequence 2, Appli	534	7	2.5	3011	5	PCT-US93-00907-2	Sequence 2, Appli
462	7	2.5	2307	4	US-09-919-901-9	Sequence 9, Appli	535	7	2.5	3011	5	PCT-US94-07280-1	Sequence 1, Appli
463	7	2.5	2307	4	US-09-919-901-16	Sequence 16, Appli	536	7	2.5	3011	5	PCT-US95-01087-1	Sequence 1, Appli
464	7	2.5	2307	4	US-10-191-966-2	Sequence 2, Appli	537	7	2.5	3012	3	US-08-811-566-2	Sequence 2, Appli
465	7	2.5	2307	4	US-10-191-966-9	Sequence 9, Appli	538	7	2.5	3012	3	US-09-034-756-2	Sequence 2, Appli

539	7	2.5	3033	1	US-07-925-695-5	Sequence 5, Appl1	612	6	2.2	72	1	US-08-217-360-10	Sequence 10, Appl1
540	7	2.5	3033	1	US-07-925-695-8	Sequence 8, Appl1	613	6	2.2	73	4	US-09-621-976-5981	Sequence 5981, Ap
541	7	2.5	3033	1	US-07-925-695-9	Sequence 9, Appl1	614	6	2.2	74	3	US-09-227-357-210	Sequence 210, App
542	6	2.2	8	4	US-09-214-307A-8	Sequence 8, Appl1	615	6	2.2	74	4	US-09-248-796A-16150	Sequence 16150, A
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544	6	2.2	12	1	US-08-410-360-2	Sequence 2, Appl1	617	6	2.2	77	4	US-09-270-767-60668	Sequence 60668, A
545	6	2.2	12	1	US-08-707-801A-2	Sequence 2, Appl1	618	6	2.2	82	4	US-09-492-709A-277	Sequence 277, App
546	6	2.2	12	1	US-08-709-006-2	Sequence 2, Appl1	619	6	2.2	85	2	US-08-222-617A-10	Sequence 10, Appl
547	6	2.2	12	1	US-08-711-175-2	Sequence 2, Appl1	620	6	2.2	85	2	US-09-198-452A-1176	Sequence 1176, Ap
548	6	2.2	13	3	US-08-782-597A-14	Sequence 14, Appl1	621	6	2.2	86	4	US-09-583-110-3661	Sequence 3661, Ap
549	6	2.2	13	3	US-09-319-730-3	Sequence 3, Appl1	622	6	2.2	87	4	US-09-732-210-957	Sequence 957, App
550	6	2.2	13	3	US-09-936-885A-20	Sequence 20, Appl1	623	6	2.2	87	4	US-09-248-796A-24914	Sequence 24914, A
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552	6	2.2	16	5	PCT-US94-01712-10	Sequence 10, Appl1	625	6	2.2	92	4	US-09-621-976-5066	Sequence 5066, Ap
553	6	2.2	21	1	US-07-946-054-5	Sequence 5, Appl1	626	6	2.2	92	4	US-09-513-999C-6075	Sequence 6075, Ap
554	6	2.2	21	5	PCT-US93-08638-5	Sequence 5, Appl1	627	6	2.2	95	4	US-09-328-352-8138	Sequence 8138, Ap
555	6	2.2	24	3	US-09-098-901-9	Sequence 9, Appl1	628	6	2.2	95	4	US-09-270-767-36636	Sequence 36636, A
556	6	2.2	29	3	US-09-045-632-52	Sequence 52, Appl1	629	6	2.2	95	4	US-09-270-767-51853	Sequence 51853, A
557	6	2.2	43	1	US-08-548-540-96	Sequence 96, Appl1	630	6	2.2	96	4	US-09-621-976-7065	Sequence 7065, Ap
558	6	2.2	43	5	PCT-US96-09809-96	Sequence 96, Appl1	631	6	2.2	98	4	US-09-107-433-4545	Sequence 4545, Ap
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560	6	2.2	47	4	US-09-902-540-11114	Sequence 11, Appl1	633	6	2.2	100	4	US-09-631-594-71	Sequence 71, Appl
561	6	2.2	48	1	US-08-548-540-92	Sequence 92, Appl1	634	6	2.2	100	4	US-09-248-796A-24980	Sequence 24980, A
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563	6	2.2	48	1	US-08-548-540-100	Sequence 100, App	636	6	2.2	101	4	US-09-902-540-11678	Sequence 11678, A
564	6	2.2	48	1	US-08-548-540-101	Sequence 101, App	637	6	2.2	102	4	US-09-902-540-15410	Sequence 15410, A
565	6	2.2	48	1	US-08-548-540-104	Sequence 104, App	638	6	2.2	103	4	US-09-270-767-57936	Sequence 57936, A
566	6	2.2	48	1	US-08-548-540-106	Sequence 106, App	639	6	2.2	105	4	US-09-710-279-82	Sequence 82, Appl
567	6	2.2	48	5	PCT-US96-09809-92	Sequence 92, Appl1	640	6	2.2	105	4	US-09-248-796A-27685	Sequence 27685, A
568	6	2.2	48	5	PCT-US96-09809-98	Sequence 98, Appl1	641	6	2.2	107	4	US-09-270-767-61201	Sequence 61201, A
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570	6	2.2	48	5	PCT-US96-09809-101	Sequence 101, App	643	6	2.2	108	4	US-09-535-852-55	Sequence 55, Appl
571	6	2.2	48	5	PCT-US96-09809-104	Sequence 104, App	644	6	2.2	109	3	US-08-466-886-26	Sequence 26, Appl
572	6	2.2	49	1	US-08-548-540-87	Sequence 87, App	645	6	2.2	109	3	US-08-469-617-26	Sequence 26, Appl
573	6	2.2	49	1	US-08-548-540-97	Sequence 97, Appl1	646	6	2.2	109	4	US-08-469-630-26	Sequence 26, Appl
574	6	2.2	49	1	US-08-548-540-99	Sequence 99, Appl1	647	6	2.2	110	1	US-08-466-886-30	Sequence 30, Appl
575	6	2.2	49	1	US-08-548-540-102	Sequence 102, App	648	6	2.2	110	1	US-08-466-886-38	Sequence 38, Appl
576	6	2.2	49	1	US-08-548-540-103	Sequence 103, App	649	6	2.2	110	3	US-08-469-617-28	Sequence 28, Appl
577	6	2.2	49	1	US-08-548-540-105	Sequence 105, App	650	6	2.2	110	3	US-08-469-617-30	Sequence 30, Appl
578	6	2.2	49	1	US-09-636-728-48	Sequence 48, Appl1	651	6	2.2	110	4	US-09-614-912-188	Sequence 188, App
579	6	2.2	49	5	PCT-US96-09809-87	Sequence 87, Appl1	652	6	2.2	110	4	US-08-469-630-28	Sequence 28, Appl
580	6	2.2	49	5	PCT-US96-09809-97	Sequence 97, Appl1	653	6	2.2	110	4	US-08-469-630-30	Sequence 30, Appl
581	6	2.2	49	5	PCT-US96-09809-99	Sequence 99, Appl1	654	6	2.2	111	1	US-08-466-886-35	Sequence 35, Appl
582	6	2.2	49	5	PCT-US96-09809-99	Sequence 99, Appl1	655	6	2.2	111	1	US-08-466-886-41	Sequence 41, Appl
583	6	2.2	49	5	PCT-US96-09809-102	Sequence 102, App	656	6	2.2	111	3	US-08-469-617-35	Sequence 35, Appl
584	6	2.2	49	5	PCT-US96-09809-103	Sequence 103, App	657	6	2.2	111	3	US-08-469-617-41	Sequence 41, Appl
585	6	2.2	49	5	PCT-US96-09809-105	Sequence 105, App	658	6	2.2	111	4	US-09-489-039A-10282	Sequence 10282, A
586	6	2.2	58	1	US-08-464-531-84	Sequence 84, Appl1	659	6	2.2	111	4	US-08-469-630-35	Sequence 35, Appl
587	6	2.2	58	1	US-08-464-531-85	Sequence 85, Appl1	660	6	2.2	111	4	US-08-469-630-41	Sequence 41, Appl
588	6	2.2	58	2	US-08-461-598-84	Sequence 84, Appl1	661	6	2.2	112	4	US-09-107-532A-5370	Sequence 5370, Ap
589	6	2.2	58	2	US-08-461-598-85	Sequence 85, Appl1	662	6	2.2	112	4	US-09-438-185A-343	Sequence 343, App
590	6	2.2	58	3	US-08-322-137-84	Sequence 85, Appl1	663	6	2.2	113	3	US-09-134-001C-2839	Sequence 2839, Ap
591	6	2.2	58	3	US-08-322-137-85	Sequence 85, Appl1	664	6	2.2	113	4	US-09-614-912-186	Sequence 186, App
592	6	2.2	59	4	US-09-270-767-6150	Sequence 40934, A	665	6	2.2	114	4	US-09-543-681A-5618	Sequence 5618, App
593	6	2.2	59	4	US-09-270-767-56150	Sequence 56150, A	666	6	2.2	114	4	US-09-513-999C-4607	Sequence 4607, Ap
594	6	2.2	61	3	US-09-107-532A-5137	Sequence 5137, Ap	667	6	2.2	115	4	US-09-252-991A-21267	Sequence 21267, A
595	6	2.2	63	4	US-09-134-000C-4119	Sequence 4119, Ap	668	6	2.2	115	4	US-09-540-236-3490	Sequence 3490, Ap
596	6	2.2	63	4	US-09-621-976-6136	Sequence 6136, Ap	669	6	2.2	116	4	US-09-902-540-13798	Sequence 13798, A
597	6	2.2	65	1	US-08-464-531-83	Sequence 83, Appl1	670	6	2.2	117	4	US-09-732-210-208	Sequence 208, App
598	6	2.2	65	2	US-08-461-598-83	Sequence 83, Appl1	671	6	2.2	118	4	US-09-673-395A-272	Sequence 272, App
599	6	2.2	65	3	US-08-322-137-83	Sequence 83, Appl1	672	6	2.2	119	4	US-09-270-767-57238	Sequence 57238, A
600	6	2.2	66	1	US-08-464-531-87	Sequence 87, Appl1	673	6	2.2	120	4	US-09-583-110-2770	Sequence 2770, Ap
601	6	2.2	66	1	US-08-464-531-88	Sequence 88, Appl1	674	6	2.2	120	4	US-09-107-433-5170	Sequence 1056, Ap
602	6	2.2	66	1	US-08-464-531-89	Sequence 88, Appl1	675	6	2.2	120	4	US-09-640-211A-1056	Sequence 6078, Ap
603	6	2.2	66	2	US-08-461-598-87	Sequence 87, Appl1	676	6	2.2	124	4	US-09-134-000C-6078	Sequence 4714, Ap
604	6	2.2	66	2	US-08-461-598-88	Sequence 88, Appl1	677	6	2.2	124	4	US-09-621-976-4714	Sequence 98, Appl
605	6	2.2	66	2	US-08-461-598-89	Sequence 89, Appl1	678	6	2.2	124	4	US-09-538-092-98	Sequence 4186, Ap
606	6	2.2	66	3	US-08-322-137-87	Sequence 87, Appl1	679	6	2.2	125	4	US-09-134-000C-4186	Sequence 37125, A
607	6	2.2	66	3	US-08-322-137-88	Sequence 88, Appl1	680	6	2.2	125	4	US-09-270-767-52342	Sequence 52342, A
608	6	2.2	66	3	US-08-322-137-89	Sequence 88, Appl1	681	6	2.2	125	4	US-09-270-767-52342	Sequence 146, App
609	6	2.2	67	4	US-09-328-352-4947	Sequence 4947, Ap	682	6	2.2	127	4	US-09-614-912-146	Sequence 4681, Ap
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687	6	2.2	132	4	US-09-248-796A-19032	Sequence 19032, A	760	6	2.2	193	4	US-09-107-532A-6802	Sequence 6802, Ap
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690	6	2.2	135	4	US-09-107-433-3822	Sequence 3822, Ap	763	6	2.2	196	1	US-08-690-095-5	Sequence 5, Appl1
691	6	2.2	136	4	US-09-252-991A-19336	Sequence 19336, A	764	6	2.2	197	3	US-09-113-789-5	Sequence 5, Appl1
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694	6	2.2	139	4	US-09-107-532A-6708	Sequence 6708, Ap	767	6	2.2	200	4	US-09-270-767-35465	Sequence 35465, A
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697	6	2.2	142	4	US-09-270-767-31819	Sequence 31819, A	770	6	2.2	203	3	US-08-858-207A-332	Sequence 332, App
698	6	2.2	143	4	US-09-248-796A-20125	Sequence 20125, A	771	6	2.2	204	4	US-09-538-092-479	Sequence 479, App
699	6	2.2	144	4	US-09-252-991A-31237	Sequence 31237, A	772	6	2.2	205	3	US-09-134-001C-4517	Sequence 4517, Ap
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703	6	2.2	148	4	US-09-710-279-2238	Sequence 2238, Ap	776	6	2.2	209	4	US-09-270-767-37440	Sequence 37440, A
704	6	2.2	149	4	US-09-513-999C-7030	Sequence 7030, Ap	777	6	2.2	210	4	US-09-270-767-42786	Sequence 42786, A
705	6	2.2	150	4	US-09-690-454-150	Sequence 150, App	778	6	2.2	211	4	US-09-270-767-5657	Sequence 52657, A
706	6	2.2	151	4	US-09-107-532A-7100	Sequence 7100, Ap	779	6	2.2	212	4	US-09-489-039A-12447	Sequence 12447, A
707	6	2.2	152	3	US-08-858-207A-433	Sequence 433, App	780	6	2.2	213	3	US-08-861-774E-38	Sequence 38, Appl1
708	6	2.2	153	4	US-09-489-039A-9682	Sequence 9682, Ap	781	6	2.2	214	4	US-09-461-325-468	Sequence 468, App
709	6	2.2	154	4	US-09-270-767-44959	Sequence 44959, A	782	6	2.2	215	4	US-09-252-991A-25390	Sequence 25390, A
710	6	2.2	155	4	US-09-107-532A-4843	Sequence 4843, Ap	783	6	2.2	216	4	US-08-956-171E-5227	Sequence 5227, Ap
711	6	2.2	156	2	US-08-414-938A-2	Sequence 2, Appl1	784	6	2.2	217	4	US-10-012-542-468	Sequence 468, App
712	6	2.2	157	4	US-09-252-991A-20956	Sequence 20956, A	785	6	2.2	218	4	US-10-115-123-468	Sequence 126, App
713	6	2.2	158	4	US-09-270-767-37121	Sequence 37121, A	786	6	2.2	219	4	US-09-893-737-126	Sequence 126, App
714	6	2.2	159	4	US-09-270-767-52338	Sequence 52338, A	787	6	2.2	220	4	US-09-252-991A-22805	Sequence 22805, A
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716	6	2.2	161	4	US-09-647-140B-30	Sequence 30, Appl1	789	6	2.2	222	4	US-09-583-110-3641	Sequence 3641, Ap
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718	6	2.2	163	4	US-09-647-140B-22	Sequence 22, Appl1	791	6	2.2	224	4	US-09-949-016-11235	Sequence 11235, A
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722	6	2.2	167	4	US-09-270-767-35638	Sequence 35638, A	795	6	2.2	228	4	US-09-583-110-4973	Sequence 4973, Ap
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732	6	2.2	177	4	US-09-614-912-134	Sequence 134, App	805	6	2.2	238	4	US-09-248-796A-23106	Sequence 23106, A
733	6	2.2	178	4	US-09-583-110-2697	Sequence 2697, Ap	806	6	2.2	239	4	US-09-134-000C-4085	Sequence 4085, Ap
734	6	2.2	179	4	US-09-248-796A-20625	Sequence 20625, A	807	6	2.2	240	4	US-09-270-767-45681	Sequence 45681, A
735	6	2.2	180	4	US-09-107-433-4797	Sequence 4797, Ap	808	6	2.2	241	4	US-09-602-787A-298	Sequence 298, App
736	6	2.2	181	4	US-09-248-796A-20163	Sequence 20163, A	809	6	2.2	242	4	US-09-602-787A-300	Sequence 300, App
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738	6	2.2	183	4	US-09-489-039A-7327	Sequence 7327, Ap	811	6	2.2	244	4	US-09-710-279-1510	Sequence 1510, Ap
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743	6	2.2	188	4	US-09-621-976-4209	Sequence 4209, Ap	816	6	2.2	249	4	US-09-543-681A-7167	Sequence 7167, Ap
744	6	2.2	189	4	US-09-252-991A-27192	Sequence 27192, A	817	6	2.2	250	2	US-09-134-000C-5879	Sequence 5879, Ap
745	6	2.2	190	4	US-09-252-991A-19743	Sequence 19743, A	818	6	2.2	251	3	US-08-471-717-2	Sequence 2, Appl1
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747	6	2.2	192	4	US-09-902-540-13108	Sequence 13108, A	820	6	2.2	253	4	US-09-614-912-164	Sequence 164, App
748	6	2.2	193	4	US-09-134-000C-4869	Sequence 4869, Ap	821	6	2.2	254	4	US-09-107-433-3620	Sequence 3620, Ap
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751	6	2.2	196	1	US-08-458-218-89	Sequence 89, Appl1	824	6	2.2	257	4		
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833	6	2.2	230	4	US-09-602-787A-472	Sequence 472, App	906	2.2	253	4	US-09-499-781-4	Sequence 4, Appli
834	6	2.2	230	4	US-09-281-646B-22	Sequence 22, Appl	907	2.2	253	4	US-09-902-540-14470	Sequence 14470, A
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839	6	2.2	233	4	US-09-583-110-2753	Sequence 2753, App	912	2.2	254	4	US-09-248-796A-20633	Sequence 20633, A
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842	6	2.2	235	4	US-09-198-452A-752	Sequence 752, App	915	2.2	255	4	US-09-433-681A-6727	Sequence 6727, App
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980 6 2.2 274 4 US-09-107-433-3393 Sequence 3393, Ap
981 6 2.2 274 4 US-09-902-540-10772 Sequence 10272, A
982 6 2.2 275 4 US-09-489-039A-7722 Sequence 7722, Ap
983 6 2.2 275 4 US-09-489-039A-12128 Sequence 12128, A
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985 6 2.2 276 4 US-09-270-767-42419 Sequence 42419, A
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988 6 2.2 277 4 US-09-107-532A-4193 Sequence 4193, Ap
989 6 2.2 278 4 US-09-489-039A-8998 Sequence 8998, Ap
990 6 2.2 279 2 US-08-326-286-7 Sequence 7, Appl
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992 6 2.2 280 4 US-09-489-039A-12451 Sequence 12451, A
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996 6 2.2 281 4 US-09-489-039A-9637 Sequence 9637, Ap
997 6 2.2 281 4 US-09-489-039A-12504 Sequence 12504, A
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ALIGNMENTS

RESULT 1
US-09-583-110-4380
; Sequence 4380, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: Pneumoniae for Diagnostics and Therapeutics
; CURRENT FILING DATE: 2000-05-26
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4380
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4380

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Best Local Similarity 100.0%; Pred. No. 1.6e-258;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-107-433-4838
; Sequence 4838, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4838:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...280
; SEQUENCE DESCRIPTION: SEQ ID NO: 4838:
US-09-107-433-4838

Query Match 95.7%; Score 267; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.6e-258;
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QY 241 EVQLGVPKITAFCCKRLADRGVSPKRLP 267
DB 242 EVQLGVPKITAFCCKRLADRGVSPKRLP 268

RESULT 3
US-09-214-307A-2
; Sequence 2, Application US/09214307A
; Patent No. 6544516
; GENERAL INFORMATION:
; APPLICANT: NEUTEC PHARMA PLC
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF INFECTIONS OF GRAM POSITIVE
; FILE REFERENCE: COCCI
; CURRENT APPLICATION NUMBER: US/09/214,307A
; PRIOR FILING DATE: 1999-01-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01830
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: GB9614274.0
; PRIOR FILING DATE: 1996-07-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-09-214-307A-2

Query Match 6.5%; Score 18; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.6e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 145 RSPFELSGGQMRRAIAG 162

RESULT 4
US-09-107-532A-6030
; Sequence 6030, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arianello, Pamela Deneke
; REGISTRATION NUMBER: 40,489

; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6030:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 284 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...284
; SEQUENCE DESCRIPTION: SEQ ID NO: 6030:
US-09-107-532A-6030
Query Match 6.5%; Score 18; DB 4; Length 284;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 141 RSPFELSGGQMRRAIAG 158
DB 152 RSPFELSGGQMRRAIAG 169

RESULT 5
US-09-134-000C-4732
; Sequence 4732, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4732
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4732

Query Match 6.1%; Score 17; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 142 SPFELSGGQMRRAIAG 158
DB 169 SPFELSGGQMRRAIAG 185

RESULT 6
US-09-861-451A-42
; Sequence 42, Application US/09861451A
; Patent No. 6759516
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific & Industrial Research Orga
; TITLE OF INVENTION: Methods of Identifying Antigen Gene Sequences
; FILE REFERENCE: FF34033/01
; CURRENT APPLICATION NUMBER: US/09/861,451A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PP7273
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42

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; LENGTH: 300
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Deduced protein
; OTHER INFORMATION: sequence from clone PAD913
US-09-861-451A-42

Query Match          3.9%; Score 11; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 RRVATAGILAM 162
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Db 165 RRVATAGILAM 175

RESULT 7
US-10-162-012-36
; Sequence 36, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 198
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-162-012-36

Query Match          3.6%; Score 10; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LDEPTAGLDP 178
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Db 146 LDEPTAGLDP 155

RESULT 8
US-09-489-039A-10009
; Sequence 10009, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709-2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10009
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10009

Query Match          3.6%; Score 10; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LDEPTAGLDP 178
    |||||
Db 167 LDEPTAGLDP 176

RESULT 9
US-09-134-001C-3292
; Sequence 3292, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3292
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3292

Query Match          3.6%; Score 10; DB 3; Length 288;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LDEPTAGLDP 178
    |||||
Db 171 LDEPTAGLDP 180
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; APPLICANT: Pompejus, Mark
; APPLICANT: Krüger, Burkhard
; APPLICANT: Schöder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/602,787A
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932190.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932191.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932927.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940765.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940766.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940830.0
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940831.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940832.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940833.5

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; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941395.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942077.7
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 352
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-602-787A-352

Query Match          3.6%; Score 10; DB 4; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LDEPTAGLDP 178
DB 150 LDEPTAGLDP 159
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RESULT 11
US-09-252-991A-21585
; Sequence 21585, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21585
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21585

Query Match          3.6%; Score 10; DB 4; Length 619;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LDEPTAGLDP 178
DB 525 LDEPTAGLDP 534
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RESULT 12
US-09-902-540-14362
; Sequence 14362, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B

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; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14362
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14362

Query Match 3.2%; Score 9; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 170 DEPTAGLDP 178
Db 159 DEPTAGLDP 167
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RESULT 13

US-09-489-039A-9627
; Sequence 9627, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9627
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9627

Query Match 3.2%; Score 9; DB 4; Length 546;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 EPAILVLDE 171
Db 445 EPAILVLDE 453
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RESULT 14

US-09-543-681A-6008
; Sequence 6008, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:

; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6008
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6008

Query Match 3.2%; Score 9; DB 4; Length 595;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GHTSGKST 48
Db 379 GHTSGKST 387
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RESULT 15

US-09-489-039A-13507
; Sequence 13507, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13507
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13507

Query Match 3.2%; Score 9; DB 4; Length 686;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GHTSGKST 48
Db 468 GHTSGKST 476
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Search completed: October 28, 2005, 18:15:42
Job time : 58 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 17:53:08 ; Search time 162 Seconds
(without alignment)
719.963 Million cell updates/sec

Title: US-09-769-744D-26

Perfect score: 1387

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Maximum DB seq length: 2000000000

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Maximum Match 100%
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Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1387	100.0	279	10	US-09-769-744A-26
2	1387	100.0	279	17	Sequence 26, Appl
3	1386	99.9	280	18	Sequence 4660, Ap
4	1378	99.4	279	9	Sequence 4838, Ap
5	1378	99.4	279	15	Sequence 13440, A
6	1002.5	72.3	280	15	US-09-815-242-13440
7	971	70.0	280	15	US-10-282-122A-74238
8	850.5	61.3	289	9	Sequence 72498, A
9	850.5	61.3	289	15	US-10-282-122A-74821
10	845.5	61.0	289	15	Sequence 10545, A
11	794	57.2	232	18	US-10-282-122A-57659
					Sequence 342, App

12	794	57.2	294	18	US-10-501-282-344
13	729	52.6	276	15	US-10-369-493-23054
14	700	50.5	293	15	US-10-282-122A-46693
15	692.5	49.9	288	15	US-10-282-122A-60478
16	683	49.2	288	15	US-10-282-122A-51996
17	661	47.7	288	15	US-10-282-122A-52691
18	637.5	45.0	282	15	US-10-369-493-17105
19	635.5	45.8	288	15	US-10-282-122A-53490
20	611	44.1	286	15	US-10-282-122A-71161
21	608	43.8	288	18	US-10-724-972A-6429
22	607	43.8	286	15	US-10-282-122A-71345
23	594.5	42.9	286	9	US-09-815-242-12234
24	589.5	42.5	286	15	US-10-282-122A-44395
25	589.5	42.5	286	17	US-10-857-625-742
26	553	39.9	272	15	US-10-282-122A-45314
27	548.5	39.5	273	9	US-09-815-242-5550
28	543	39.1	180	14	US-10-054-968-2
29	540.5	39.0	304	15	US-10-282-122A-63497
30	533.5	38.5	303	15	US-10-282-122A-64291
31	508	36.6	300	9	US-09-861-451A-42
32	489.5	35.3	277	15	US-10-282-122A-53483
33	486	35.0	273	15	US-10-369-493-16472
34	485	35.0	279	15	US-10-282-122A-52131
35	484.5	34.9	285	15	US-10-282-122A-52539
36	484	34.9	300	15	US-10-282-122A-45307
37	483.5	34.9	281	15	US-10-282-122A-52154
38	479	34.5	279	15	US-10-282-122A-60654
39	468.5	33.8	279	15	US-10-282-122A-57649
40	457	32.9	433	15	US-10-282-122A-76895
41	454.5	32.8	279	15	US-10-282-122A-57249
42	454.5	32.8	291	9	US-09-815-242-10544
43	452	32.6	279	18	US-10-501-282-346
44	431.5	31.1	274	15	US-10-282-122A-64292
45	424.5	30.6	296	15	US-10-282-122A-74822

ALIGNMENTS

RESULT 1

US-09-769-744A-26
; Sequence 26, Application US/09769744A
; Publication No. US20030134407A1
; GENERAL INFORMATION:
; APPLICANT: Le Page, Richard WF
; APPLICANT: Wells, Jeremy M
; APPLICANT: Hanniffy, Sean B
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21122WO
; CURRENT APPLICATION NUMBER: US/09/769,744A
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/GB99/02452
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: GB 9816336.3
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: US 60/125329
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-769-744A-26

Query Match 100.0%; Score 1387; DB 10; Length 279;
Best Local Similarity 100.0%; Pred. No. 2.1e-122;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MGIALENVNTYQEGTPLASALSDVSLTDCSYTALIGHTSGKSTLQLLGLVPS 60
1 MGIALENVNTYQEGTPLASALSDVSLTDCSYTALIGHTSGKSTLQLLGLVPS 60

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QY 61 QGSRVFDLTITSTSKNDIRQIRKQVGLVQFAENQIFBETVLKDVAFGPNFGVSEED 120
DB 61 QGSRVFDLTITSTSKNDIRQIRKQVGLVQFAENQIFBETVLKDVAFGPNFGVSEED 120
QY 121 AVKTAREKALVIGIDESLFDSPFELSGQMRRAIAGILAMEPAAILVLDEPTAGLDPLG 180
DB 121 AVKTAREKALVIGIDESLFDSPFELSGQMRRAIAGILAMEPAAILVLDEPTAGLDPLG 180
QY 181 RKELMTLTKLHQSGMTIVLVTHLMDVVAEVANQVYVMEKGLVKGKPSDVFDQVWFME 240
DB 181 RKELMTLTKLHQSGMTIVLVTHLMDVVAEVANQVYVMEKGLVKGKPSDVFDQVWFME 240
QY 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279
DB 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279
```

RESULT 2

```
US-10-472-928-4660
; Sequence 4660, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026926W0
; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4660
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; OTHER INFORMATION: ABC transporter, ATP-binding protein
; OTHER INFORMATION: Cellular location: membrane
; OTHER INFORMATION: Similar to strain R6 sequence 15904066 (e-154)
US-10-472-928-4660
```

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Query Match 100.0%; Score 1387; DB 17; Length 279;
Best Local Similarity 100.0%; Pred. No. 2.1e-122;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGIALENVNTYQSGTPLASALSDVSLTIEDGSYTALIGHTSGKSTILQLLGLLVPS 60
DB 1 MGIALENVNTYQSGTPLASALSDVSLTIEDGSYTALIGHTSGKSTILQLLGLLVPS 60
QY 61 QGSRVFDLTITSTSKNDIRQIRKQVGLVQFAENQIFBETVLKDVAFGPNFGVSEED 120
DB 61 QGSRVFDLTITSTSKNDIRQIRKQVGLVQFAENQIFBETVLKDVAFGPNFGVSEED 120
QY 121 AVKTAREKALVIGIDESLFDSPFELSGQMRRAIAGILAMEPAAILVLDEPTAGLDPLG 180
DB 121 AVKTAREKALVIGIDESLFDSPFELSGQMRRAIAGILAMEPAAILVLDEPTAGLDPLG 180
QY 181 RKELMTLTKLHQSGMTIVLVTHLMDVVAEVANQVYVMEKGLVKGKPSDVFDQVWFME 240
DB 181 RKELMTLTKLHQSGMTIVLVTHLMDVVAEVANQVYVMEKGLVKGKPSDVFDQVWFME 240
QY 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279
DB 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279
```

RESULT 3

```
US-10-617-320-4838
; Sequence 4838, Application US/10617320
; Publication No. US20050136404A1
; GENERAL INFORMATION:
```

```
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/617,320
FILING DATE: 10-Jul-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4838:
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...280
SEQUENCE DESCRIPTION: SEQ ID NO: 4838:
US-10-617-320-4838
```

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Query Match 99.9%; Score 1386; DB 18; Length 280;
Best Local Similarity 99.6%; Pred. No. 2.6e-122;
Matches 278; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGIALENVNTYQSGTPLASALSDVSLTIEDGSYTALIGHTSGKSTILQLLGLLVPS 60
DB 2 MGIALENVNTYQSGTPLASALSDVSLTIEDGSYTALIGHTSGKSTILQLLGLLVPS 61
QY 61 QGSRVFDLTITSTSKNDIRQIRKQVGLVQFAENQIFBETVLKDVAFGPNFGVSEED 120
DB 62 QGSRVFDLTITSTSKNDIRQIRKQVGLVQFAENQIFBETVLKDVAFGPNFGVSEED 121
QY 121 AVKTAREKALVIGIDESLFDSPFELSGQMRRAIAGILAMEPAAILVLDEPTAGLDPLG 180
DB 122 AVKTAREKALVIGIDESLFDSPFELSGQMRRAIAGILAMEPAAILVLDEPTAGLDPLG 181
QY 181 RKELMTLTKLHQSGMTIVLVTHLMDVVAEVANQVYVMEKGLVKGKPSDVFDQVWFME 240
DB 182 RKELMTLTKLHQSGMTIVLVTHLMDVVAEVANQVYVMEKGLVKGKPSDVFDQVWFME 241
QY 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279
DB 242 EVQLGVPKITAFCKRLADRGVSFKRLPVKIEFKESLNG 280
```

RESULT 4

US-09-815-242-13440
; Sequence 13440, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 13440
; LENGTH: 279
; TYPE: PRF
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13440

Query Match 99.4%; Score 1378; DB 9; Length 279;
Best Local Similarity 99.3%; Pred. No. 1.5e-121;
Matches 277; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGIALENNVFTYQEGTPLASAAALSDVSLTIEDGSGYALIGHTGSGKSTILQINGLLVPS 60
DB 1 MGIALENNVFTYQEGTPLASAAALSDVSLTIEDGSGYALIGHTGSGKSTILQINGLLVPS 60
QY 61 QGSVRVPDTLITSTSKNKDIQIRKQVGLVFPQFAENQIPEETVLKDVAFGPQNGVSEED 120
DB 61 QGSVRVPDTLITSTSKNKDIQIRKQVGLVFPQFAENQIPEETVLKDVAFGPQNGVSEED 120
QY 121 AVKTAREKALVGDLSLDFDRSPFELSGGOMRRVAIAGILAMEPAILVLDDEPTAGLDPLG 180
DB 121 AVKTAREKALVGDLSLDFDRSPFELSGGOMRRVAIAGILAMEPAILVLDDEPTAGLDPLG 180
QY 181 RKELMTLTKKLHQSGMTIVLVTHLMDVDAEYANQVYVMEKGRVLKGGKPSDVFQDVVFM 240
DB 181 RKELMTLTKKLHQSGMTIVLVTHLMDVDAEYANQVYVMEKGRVLKGGKPSDVFQDVVFM 240
QY 241 EVQLGVPKITAFCCKRLADRGVSPKRLPIKIEEFKESLNG 279
DB 241 EVQLGVPKITAFCCKRLADRGVSPKRLPIKIEEFKESLNG 279

RESULT 5

US-10-282-122A-74238
; Sequence 74238, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74238
; LENGTH: 279
; TYPE: PRF
; ORGANISM: Streptococcus pneumoniae
US-10-282-122A-74238

Query Match 99.4%; Score 1378; DB 15; Length 279;
Best Local Similarity 99.3%; Pred. No. 1.5e-121;
Matches 277; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGIALENNVFTYQEGTPLASAAALSDVSLTIEDGSGYALIGHTGSGKSTILQINGLLVPS 60
DB 1 MGIALENNVFTYQEGTPLASAAALSDVSLTIEDGSGYALIGHTGSGKSTILQINGLLVPS 60
QY 61 QGSVRVPDTLITSTSKNKDIQIRKQVGLVFPQFAENQIPEETVLKDVAFGPQNGVSEED 120
DB 61 QGSVRVPDTLITSTSKNKDIQIRKQVGLVFPQFAENQIPEETVLKDVAFGPQNGVSEED 120
QY 121 AVKTAREKALVGDLSLDFDRSPFELSGGOMRRVAIAGILAMEPAILVLDDEPTAGLDPLG 180
DB 121 AVKTAREKALVGDLSLDFDRSPFELSGGOMRRVAIAGILAMEPAILVLDDEPTAGLDPLG 180
QY 181 RKELMTLTKKLHQSGMTIVLVTHLMDVDAEYANQVYVMEKGRVLKGGKPSDVFQDVVFM 240
DB 181 RKELMTLTKKLHQSGMTIVLVTHLMDVDAEYANQVYVMEKGRVLKGGKPSDVFQDVVFM 240
QY 241 EVQLGVPKITAFCCKRLADRGVSPKRLPIKIEEFKESLNG 279
DB 241 EVQLGVPKITAFCCKRLADRGVSPKRLPIKIEEFKESLNG 279

RESULT 6

US-10-282-122A-72498
; Sequence 72498, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

```
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Foreyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 72498
/ LENGTH: 280
/ TYPE: PRT
/ ORGANISM: Streptococcus mutans
US-10-282-122A-72498

Query Match      72.3%; Score 1002.5; DB 15; Length 280;
Best Local Similarity 70.0%; Pred. No. 4.4e-86;
Matches 196; Conservative 38; Mismatches 45; Indels 1; Gaps 1;

QY 1 MGIALENVFTYQGTPLASAAALSDVSLTIEDGYSYTAUGHTGSGKSTILQLLNGLLVPS 60
DB 1 MGINLQVSVTYQAGTPPEGRALFNVSLEIKDGSFTAFIGHTGSGKSTIMQLLNGLTPT 60
QY 61 QGSVRVFTLTSTSKNDIRKQVGLVFOFAENQIFETVLKDVAFGPNQFVSEED 120
DB 61 EGTVLVDVDAIRSDSKNDIRKQVGLVFOFPESQLFDETVLKDVPAGPNQFVSEED 120
QY 121 AVKTAREKALVIGIDESLFDSPFELSGQMRVAIAGILAMEPAAILVLDEPTAGLDPLG 180
DB 121 AEKLAREKALVIGISEELFEKNPFELSGQMRVAIAGILAMEPAAILVLDEPTAGLDPLG 180
QY 181 RKEMLTLFKKLHQSGMTIVLVTHLMDVDAEYANQVYVMEKGRVLKGGKSPDVQDVPMFE 240
DB 181 RRELMTLFLKELHQSGMTIVLVTHLMDVDAEYANQVYVMEKGRVLKGGKSPDVQDVPMFE 240
QY 241 EVQLGVPKITAFCRLADRGVSKFLPIKIEEFKESL-NG 279
DB 241 SKQLGVPKITQPAHLRKGITFDALPTLLEEFVEAINGK 280
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RESULT 7

US-10-282-122A-74821

/ Sequence 74821, Application US/10282122A

```
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Foreyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 74821
/ LENGTH: 280
/ TYPE: PRT
/ ORGANISM: Streptococcus pyogenes
US-10-282-122A-74821

Query Match      70.0%; Score 971; DB 15; Length 280;
Best Local Similarity 69.0%; Pred. No. 4.2e-83;
Matches 191; Conservative 35; Mismatches 51; Indels 0; Gaps 0;

QY 1 MGIALENVFTYQGTPLASAAALSDVSLTIEDGYSYTAUGHTGSGKSTILQLLNGLLVPS 60
DB 1 MSINLQVSVTYQAGTPPEGRALFNINLIDGYSYTAUGHTGSGKSTIMQLLNGLVPT 60
QY 61 QGSVRVFTLTSTSKNDIRKQVGLVFOFAENQIFETVLKDVAFGPNQFVSEED 120
DB 61 TGISVVDKQDITNHSKNDIRKQVGLVFOFPESQLFDETVLKDVPAGPNQFVSEED 120
QY 121 AVKTAREKALVIGIDESLFDSPFELSGQMRVAIAGILAMEPAAILVLDEPTAGLDPLG 180
DB 121 AEKLAREKALVIGISEELFEKNPFELSGQMRVAIAGILAMEPAAILVLDEPTAGLDPLG 180
QY 181 RKEMLTLFKKLHQSGMTIVLVTHLMDVDAEYANQVYVMEKGRVLKGGKSPDVQDVPMFE 240
DB 181 RKEMLTLFKKLHQSGMTIVLVTHLMDVDAEYANQVYVMEKGRVLKGGKSPDVQDVPMFE 240
QY 241 EVQLGVPKITAFCRLADRGVSKFLPIKIEEFKESL 277
DB 241 KKQLGVPKITQPAHLRKGITFDALPTLLEEFVEAL 277

RESULT 8
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US-09-815-242-10545	
; Sequence 10545, Application US/09815242	
; Patent No. US20020061569A1	
; GENERAL INFORMATION:	
; APPLICANT: Haselbeck, Robert	
; APPLICANT: Ohlsen, Kari L.	
; APPLICANT: Zyskind, Judith W.	
; APPLICANT: Wall, Daniel	
; APPLICANT: Trawick, John D.	
; APPLICANT: Carr, Grant J.	
; APPLICANT: Yamamoto, Robert T.	
; APPLICANT: Xu, H. Howard	
; TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes	
; FILE REFERENCE: ELITRA.011A	
; CURRENT APPLICATION NUMBER: US/09/815,242	
; CURRENT FILING DATE: 2001-03-21	
; PRIOR APPLICATION NUMBER: 60/191,078	
; PRIOR FILING DATE: 2000-03-21	
; PRIOR APPLICATION NUMBER: 60/206,848	
; PRIOR FILING DATE: 2000-05-23	
; PRIOR APPLICATION NUMBER: 60/207,727	
; PRIOR FILING DATE: 2000-05-26	
; PRIOR APPLICATION NUMBER: 60/242,578	
; PRIOR FILING DATE: 2000-10-23	
; PRIOR APPLICATION NUMBER: 60/253,625	
; PRIOR FILING DATE: 2000-11-27	
; PRIOR APPLICATION NUMBER: 60/257,931	
; PRIOR FILING DATE: 2000-12-22	
; PRIOR APPLICATION NUMBER: 60/269,308	
; PRIOR FILING DATE: 2001-02-16	
; NUMBER OF SEQ ID NOS: 1410	
; SOFTWARE: FastSeq for Windows Version 4.0	
; SEQ ID NO 10545	
; LENGTH: 289	
; TYPE: PRT	
; ORGANISM: Enterococcus faecalis	
US-09-815-242-10545	
Query Match 61.3%; Score 850.5; DB 9; Length 289;	
Best Local Similarity 57.9%; Pred. No. 1.1e-71;	
Matches 161; Conservative 54; Mismatches 62; Indels 1; Gaps 1;	
QY 1	MGIALENVFTYQEGTPLASALSDVSLTIEDGSYTALIGHTSGSKSTIOLLNGLVPS 60
DB 1	MDIRFKQVDFTYQNTPFQEQALFDINLTIQDGSYTAIVGHTSGSKSTLLQHLNALVKPT 60
QY 61	QGSVRVFDTLTSTSKNKDIQIRKQVGLVQFAENQIPEETVLKDVAFQPNFGVSEED 120
DB 61	KGQVTIGERVITPDTDNKLNKPIRKKGIVGFQPEAQLFEETVERDIAFGPKNFGVSD 120
QY 121	AVKTAREKALVGIDSLFDRSPFELSGGQMRRAVATAGILAMEPAILVLDDEPTAGLDPLG 180
DB 121	AKKLAKMLDLVGLDEKYLQHSFPFELSGGQMRRAVATAGILAMEPEVLVLDDEPTAGLDPKG 180
QY 181	RKELMTLFFKLH-QSGMTIVLVTHLMDDDVAEYANOVYVMEKGRLVKGGKSDVFDVVF 239
DB 181	RKEMMEMFSRLHKEHNMTIVLVTHLMDDDVANYADHVILVLEKQIVRAGAPQEVFQEQWL 240
QY 240	EEVQLGVPKITAFCKRLADRGVSFKRLPIKIEEFKESL 277
DB 241	KEQLGVPTAAEFAEKLVAKGFSFEQLPLTADQLADQL 278
RESULT 9	
US-10-282-122A-57248	
; Sequence 57248, Application US/10282122A	
; Publication No. US20040029129A1	
; GENERAL INFORMATION:	
; APPLICANT: Wang, Liangsu	
; APPLICANT: Zamudio, Carlos	
; APPLICANT: Malone, Cheryl	
; APPLICANT: Haselbeck, Robert	
US-10-282-122A-57248	
Query Match 61.3%; Score 850.5; DB 15; Length 289;	
Best Local Similarity 57.9%; Pred. No. 1.1e-71;	
Matches 161; Conservative 54; Mismatches 62; Indels 1; Gaps 1;	
QY 1	MGIALENVFTYQEGTPLASALSDVSLTIEDGSYTALIGHTSGSKSTIOLLNGLVPS 60
DB 1	MDIRFKQVDFTYQNTPFQEQALFDINLTIQDGSYTAIVGHTSGSKSTLLQHLNALVKPT 60
QY 61	QGSVRVFDTLTSTSKNKDIQIRKQVGLVQFAENQIPEETVLKDVAFQPNFGVSEED 120
DB 61	KGQVTIGERVITPDTDNKLNKPIRKKGIVGFQPEAQLFEETVERDIAFGPKNFGVSD 120
QY 121	AVKTAREKALVGIDSLFDRSPFELSGGQMRRAVATAGILAMEPAILVLDDEPTAGLDPLG 180
DB 121	AKKLAKMLDLVGLDEKYLQHSFPFELSGGQMRRAVATAGILAMEPEVLVLDDEPTAGLDPKG 180
QY 181	RKELMTLFFKLH-QSGMTIVLVTHLMDDDVAEYANOVYVMEKGRLVKGGKSDVFDVVF 239
DB 181	RKEMMEMFSRLHKEHNMTIVLVTHLMDDDVANYADHVILVLEKQIVRAGAPQEVFQEQWL 240
QY 240	EEVQLGVPKITAFCKRLADRGVSFKRLPIKIEEFKESL 277
DB 241	KEQLGVPTAAEFAEKLVAKGFSFEQLPLTADQLADQL 278
RESULT 10	
US-10-282-122A-57659	
; Sequence 57659, Application US/10282122A	
; Publication No. US20040029129A1	
; GENERAL INFORMATION:	
; APPLICANT: Wang, Liangsu	
; APPLICANT: Zamudio, Carlos	
; APPLICANT: Xu, H.	
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms	
; FILE REFERENCE: ELITRA.034A	
; CURRENT APPLICATION NUMBER: US/10/282,122A	
; CURRENT FILING DATE: 2003-02-20	
; PRIOR APPLICATION NUMBER: 60/191,078	
; PRIOR FILING DATE: 2000-03-21	
; PRIOR APPLICATION NUMBER: 60/206,848	
; PRIOR FILING DATE: 2000-05-23	
; PRIOR APPLICATION NUMBER: 60/207,727	
; PRIOR FILING DATE: 2000-05-26	
; PRIOR APPLICATION NUMBER: 60/230,335	
; PRIOR FILING DATE: 2000-09-06	
; PRIOR APPLICATION NUMBER: 60/230,347	
; PRIOR FILING DATE: 2000-09-09	
; PRIOR APPLICATION NUMBER: 60/242,578	
; PRIOR FILING DATE: 2000-10-23	
; PRIOR APPLICATION NUMBER: 60/253,625	
; PRIOR FILING DATE: 2000-11-27	
; PRIOR APPLICATION NUMBER: 60/257,931	
; PRIOR FILING DATE: 2000-12-22	
; PRIOR APPLICATION NUMBER: 60/267,636	
; PRIOR FILING DATE: 2001-02-09	
; PRIOR APPLICATION NUMBER: 60/269,308	
; PRIOR FILING DATE: 2001-02-16	
; Remaining Prior Application data removed - See File Wrapper or PALM.	
; NUMBER OF SEQ ID NOS: 78614	
; SOFTWARE: Patentin version 3.1	
; SEQ ID NO 57248	
; LENGTH: 289	
; TYPE: PRT	
; ORGANISM: Enterococcus faecalis	
US-10-282-122A-57248	
Query Match 61.3%; Score 850.5; DB 15; Length 289;	
Best Local Similarity 57.9%; Pred. No. 1.1e-71;	
Matches 161; Conservative 54; Mismatches 62; Indels 1; Gaps 1;	
QY 1	MGIALENVFTYQEGTPLASALSDVSLTIEDGSYTALIGHTSGSKSTIOLLNGLVPS 60
DB 1	MDIRFKQVDFTYQNTPFQEQALFDINLTIQDGSYTAIVGHTSGSKSTLLQHLNALVKPT 60
QY 61	QGSVRVFDTLTSTSKNKDIQIRKQVGLVQFAENQIPEETVLKDVAFQPNFGVSEED 120
DB 61	KGQVTIGERVITPDTDNKLNKPIRKKGIVGFQPEAQLFEETVERDIAFGPKNFGVSD 120
QY 121	AVKTAREKALVGIDSLFDRSPFELSGGQMRRAVATAGILAMEPAILVLDDEPTAGLDPLG 180
DB 121	AKKLAKMLDLVGLDEKYLQHSFPFELSGGQMRRAVATAGILAMEPEVLVLDDEPTAGLDPKG 180
QY 181	RKELMTLFFKLH-QSGMTIVLVTHLMDDDVAEYANOVYVMEKGRLVKGGKSDVFDVVF 239
DB 181	RKEMMEMFSRLHKEHNMTIVLVTHLMDDDVANYADHVILVLEKQIVRAGAPQEVFQEQWL 240
QY 240	EEVQLGVPKITAFCKRLADRGVSFKRLPIKIEEFKESL 277
DB 241	KEQLGVPTAAEFAEKLVAKGFSFEQLPLTADQLADQL 278
APPLICANT: Ohlsen, Kari	
APPLICANT: Zyskind, Judith	
APPLICANT: Wall, Daniel	
APPLICANT: Trawick, John	
APPLICANT: Carr, Grant	
APPLICANT: Yamamoto, Robert	
APPLICANT: Forsyth, R.	
APPLICANT: Xu, H.	

```
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57659
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-10-282-122A-57659

Query Match 61.0%; Score 845.5; DB 15; Length 289;
Best Local Similarity 58.3%; Pred. No. 3.1e-71;
Matches 162; Conservative 53; Mismatches 62; Indels 1; Gaps 1;

Qy 1 MGIALENVFTYQGTPLASALS DSVSLTIEDGSYTALIGHTSGKSTILQLLGLLVPS 60
Db 1 MDIRPEQVDFTYQNTPEQRALPDINMTIKENSYTALVGHGTSGKSTILQLLGLLVKPT 60

Qy 61 QGSVRVFTLTSTSKNDIRQIRKQVGLVQPAENQIPETVLDKVAFGPNFGVSEED 120
Db 61 SGTVHIGERDIPQTDNKNLKPIRKKVGIVQFPEAQLFEETVANDIAFGPKNFGVSEEE 120

Qy 121 AVKTAREKALVGDIESLFDSPPELGGQRRVAIGALAMEPAILVLDPTAGLDPLG 180
Db 121 ALVLAKETLEQGLDESYLESPPELGGQRRVAIGALVAMPPEVLVDPTAGLDPLG 180

Qy 181 RKELMTLTKKLH-QSGMTIVLTVHLMDDVAEYANQVYVMEKGRLVKGGKPSDVFQDVVFM 239
Db 181 RKENMEMPRWLHKEQQIITVLTVHLMDDVANPADVYVYVLEKGRIVNSGEPQEVFNIEWL 240

Qy 240 EVOVLGVPKITAFCKRLADRGVSFKRLPIKIEEFKESL 277
Db 241 KEKQLGVPTATSFABELMAKGNFATLPLTABELADAI 278

RESULT 11
US-10-501-282-342
; Sequence 342, Application US/10501282
; Publication No. US20050203280A1
; GENERAL INFORMATION:
; APPLICANT: MCMICHAEL, JOHN CALHOUN
; APPLICANT: ZAGURSKY, ROBERT JOHN
; APPLICANT: RUSSELL, DAVID PARRISH
; APPLICANT: FLETCHER, LEAH DIANE
; TITLE OF INVENTION: ALLOILOCOCCLUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
; FILE REFERENCE: AM100780 L2
; CURRENT APPLICATION NUMBER: US/10/501,282
; CURRENT FILING DATE: 2004-07-09
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/426,742
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/36123
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 6653
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 344
; LENGTH: 294
; TYPE: PRT
```

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; APPLICANT: MCMICHAEL, JOHN CALHOUN
; APPLICANT: ZAGURSKY, ROBERT JOHN
; APPLICANT: RUSSELL, DAVID PARRISH
; APPLICANT: FLETCHER, LEAH DIANE
; TITLE OF INVENTION: ALLOILOCOCCLUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
; FILE REFERENCE: AM100780 L2
; CURRENT APPLICATION NUMBER: US/10/501,282
; CURRENT FILING DATE: 2004-07-09
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/333,777
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/426,742
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/36123
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 6653
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 342
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Alloiococcus otitidis
US-10-501-282-342

Query Match 57.2%; Score 794; DB 18; Length 292;
Best Local Similarity 54.1%; Pred. No. 2.3e-66;
Matches 151; Conservative 62; Mismatches 64; Indels 2; Gaps 2;

Qy 1 MGIALENVFTYQGTPLASALS DSVSLTIEDGSYTALIGHTSGKSTILQLLGLLVPS 60
Db 1 MDIRFQEVGFTYQGTTPESRALYDINLSIKGSYTALVGHGTSGKSTVLQHLNALKIPT 60

Qy 61 QGSVRVFTLTSTSKNDIRQIRKQVGLVQPAENQIPETVLDKVAFGPNFGVSEED 120
Db 61 EGQVHIGDRVISQESENKKLAKKKVGIVQFPEAQLFEETVQGDIAFGPKNFGKSOEE 120

Qy 121 AVKTAREKALVGDIESLFDSPPELGGQRRVAIGALAMEPAILVLDPTAGLDPLG 180
Db 121 ADDIVQDMLLVGLDESFRDRSPDLGGQRRVAIGALVQLPEVLVDPTAGLDPLG 180

Qy 181 RKELMTLTKKLH-QSGMTIVLTVHLMDDVAEYANQVYVMEKGRLVKGGKPSDVFQDVVFM 239
Db 181 RQETMDMFYKLHKEGLTIVLTVHLMDDVADYADHMTVLDHGTVKREGQPREIFKEADWL 240

Qy 240 EVOVLGVPKITAFCKRLADRGVSFKRLPIKIEEFKESL 277
Db 241 NSLKLGLPKSVRFANRLQKSEFGWDFDLPLTTEELGQAI 279

RESULT 12
US-10-501-282-344
; Sequence 344, Application US/10501282
; Publication No. US20050203280A1
; GENERAL INFORMATION:
; APPLICANT: MCMICHAEL, JOHN CALHOUN
; APPLICANT: ZAGURSKY, ROBERT JOHN
; APPLICANT: RUSSELL, DAVID PARRISH
; APPLICANT: FLETCHER, LEAH DIANE
; TITLE OF INVENTION: ALLOILOCOCCLUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
; FILE REFERENCE: AM100780 L2
; CURRENT APPLICATION NUMBER: US/10/501,282
; CURRENT FILING DATE: 2004-07-09
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/333,777
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/426,742
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/36123
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 6653
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 344
; LENGTH: 294
; TYPE: PRT
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 17:35:21 ; Search time 40 Seconds
(without alignments)
671.112 Million cell updates/sec

Title: US-09-769-744D-26
Perfect score: 1387
Sequence: 1 MGIALENVNFYQEGTPLAS.....GVSFKRLPIKIEEFKESLNG 279

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pirl:.*
2: Pirl2:.*
3: Pirl3:.*
4: Pirl4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1387	100.0	279	2 C95259	ABC transporter, A
2	1378	99.4	279	2 F98124	hypothetical prote
3	899.5	64.9	288	2 F86659	ABC transporter Ar
4	729	52.6	276	2 B69742	ABC transporter (A
5	696.5	50.2	288	2 AG1775	ABC transporter (A
6	692.5	49.9	288	2 AH1399	ABC transporter (A
7	683	49.2	286	2 F97281	ABC-type transport
8	637.5	46.0	282	2 E83670	ABC transporter (A
9	595.5	42.9	304	2 C90360	ABC transporter at
10	589.5	42.5	286	2 H90018	hypothetical prote
11	540.5	39.0	304	2 I64219	membrane transport
12	533.5	38.5	303	2 S62814	histidine transport
13	511.5	36.9	279	2 G64435	cobalt transport A
14	485	35.0	279	2 E97068	cobalt transport (
15	484	34.9	278	2 T44412	ABC transporter (A
16	483.5	34.9	281	2 G97281	ABC-type transport
17	479	34.5	279	2 AI1399	ABC transporter (A
18	473	34.1	311	2 A69095	cobalt transport A
19	465	33.5	279	2 AH1775	ABC transporter (A
20	464	33.5	277	2 T45265	cobalt transport A
21	457.5	33.0	280	2 G69043	cobalt transport A
22	457	32.9	433	2 D82879	ABC transporter UU
23	456.5	32.9	280	2 H75151	abc transporter, A
24	443	31.9	260	2 B71234	probable transport
25	436.5	31.5	281	2 E69751	ABC transporter (A
26	435.5	31.4	266	2 A72401	ABC transporter, A
27	431.5	31.1	274	2 S62815	sulfate transport
28	431.5	31.1	284	2 G71192	probable cobalt tr
29	429.5	31.0	280	2 T03543	probable cobalt tr

ALIGNMENTS

RESULT 1

C95259
ABC transporter, ATP-binding protein SP2220 [imported] - Streptococcus pneumoniae (strain C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 16-Aug-2004
C;Accession: C95259
R;Tetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidn on, J.D.; Hickey, E.K.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel, I nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: C95259
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-279 <KUR>
A;Cross-references: UNIPROT:Q97N51; GB:AB005672; PIDN:AAK76268.1; PID:g14973730; GSPDB:G A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP2220
C;Superfamily: ATP-binding cassette homology

Query Match	100.0%;	Score 1387;	DB 2;	Length 279;
Best Local Similarity	100.0%;	Pred. No. 9.8e-97;		
Matches 279;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGIALENVNFYQEGTPLASAA	SDVSLTIEDGSGY	TALIGHTGSGKSTILQLLGLVPS 60
Db	1	MGIALENVNFYQEGTPLASAA	SDVSLTIEDGSGY	TALIGHTGSGKSTILQLLGLVPS 60
QY	61	QGSVRVFDTLITSTSKNKDI	RQIRKQVGLVQFAENQI	FEETVLKDVAFQPNFVSEED 120
Db	61	QGSVRVFDTLITSTSKNKDI	RQIRKQVGLVQFAENQI	FEETVLKDVAFQPNFVSEED 120
QY	121	AVKTAREKALVGDLSLDRSP	FFELSGGQRRVAIAGILAM	EPAILVLEDEPTAGLDPLG 180
Db	121	AVKTAREKALVGDLSLDRSP	FFELSGGQRRVAIAGILAM	EPAILVLEDEPTAGLDPLG 180
QY	181	RKELMTLTKKLHQS	GMTIVLVTHLMDDAV	EYANQVYVMEKGRLVKGGKPSDVFQDVVME 240
Db	181	RKELMTLTKKLHQS	GMTIVLVTHLMDDAV	EYANQVYVMEKGRLVKGGKPSDVFQDVVME 240
QY	241	EVQLGVPKITAFC	KRLADRGVSFKRLPIKIEE	FKESLNG 279
Db	241	EVQLGVPKITAFC	KRLADRGVSFKRLPIKIEE	FKESLNG 279

RESULT 2

F98124
hypothetical protein ABC-NBP [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae

C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 16-Aug-2004
C/Accession: F98124
R/Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A37872; MUID:21429245; PMID:11544234
A/Accession: F98124
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-279 <KUN>
A/Cross-references: UNIPROT:Q8DMY0; GB:AE007317; PIDN:AAL00827.1; PID:gl15459731; GSPDB:C
C/Genetics:
A/Gene: ABC-NBP
C/Superfamily: ATP-binding cassette homology

Query Match 99.4%; Score 1378; DB 2; Length 279;
Best Local Similarity 99.3%; Pred. No. 4.7e-96;
Matches 277; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGIALENVFTYQEGTPLASALSVDLSLTIEDGSGTALIGHTSGKSTILQLLGLLVPS 60
Db 1 MGIALENVFTYQEGTPLASALSVDLSLTIEDGSGTALIGHTSGKSTILQLLGLLVPS 60

Qy 61 QGSVRVFDLTITSTSKNDIRQIRKQVGLVGFQFAENQIFETVLKDVAFGPNQFVSEED 120
Db 61 QGSVRVFDLTITSTSKNDIRQIRKQVGLVGFQFAENQIFETVLKDVAFGPNQFVSEED 120

Qy 121 AVKTAREKALVIGIDESLFDSPFELSGQMRRAIAGILAMEPAILVLDEPTAGLDPLG 180
Db 121 AVKTAREKALVIGIDESLFDSPFELSGQMRRAIAGILAMEPAILVLDEPTAGLDPLG 180

Qy 181 RKELMTLPKLLHQSGMTIVLVTHLMDVAVYANQVYVMEKGRVKGKPSDVDFQVFWME 240
Db 181 RKELMTLPKLLHQSGMTIVLVTHLMDVAVYANQVYVMEKGRVKGKPSDVDFQVFWME 240

Qy 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279
Db 241 EVQLGVPKITAFCKRLADRGVSFKRLPIKIEFKESLNG 279

RESULT 3
F86659
ABC transporter ATP-binding protein yche [imported] - Lactococcus lactis subsp. lactis
C/Species: Lactococcus lactis subsp. lactis
C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 16-Aug-2004
C/Accession: F86659
R/Solotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A/Reference number: A86625; MUID:21235186; PMID:11337471
A/Accession: F86659
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-288 <STO>
A/Cross-references: UNIPROT:Q9CIS8; GB:AE005176; PID:gl12723140; PIDN:AAK04376.1; GSPDB:C
A/Experimental source: strain IL1403
C/Genetics:
A/Gene: yche
C/Superfamily: ATP-binding cassette homology

Query Match 64.9%; Score 899.5; DB 2; Length 288;
Best Local Similarity 64.8%; Pred. No. 3.7e-60;
Matches 173; Conservative 46; Mismatches 47; Indels 1; Gaps 1;

Qy 3 IALENVNFTYQEGTPLASALSVDLSLTIEDGSGTALIGHTSGKSTILQLLGLLVPSQ 62
Db 2 IKFEKNVNTYQNSPFAGRALFDLKVKGSGSYTALIGHTSGKSTILQLLGLLVPSQ 61

Qy 63 SVRVFDLTITSTSKNDIRQIRKQVGLVGFQFAENQIFETVLKDVAFGPNQFVSEEDAV 122

Db 62 TVRVGDIVVTSTSKQKIKPVRKKVGVVFPQSPESQLFEETVLKDVAFGPNQFNGISKEBAE 121

Qy 123 KTAREKALVIGIDESLFDSPFELSGQMRRAIAGILAMEPAILVLDEPTAGLDPLGRK 182
Db 122 KIAAEKLEWGLSKEFEWKSPELSCGQMRRAIAGILAMEPEVLVLDEPTAGLDPKARI 181

Qy 183 ELMTLPKLLHQSGMTIVLVTHLMDVAVYANQVYVMEKGRVKGKPSDVDFQVFWMESEV 242
Db 182 EMKMLFESIHTGTGVVTLVTHLMDVADYADYVLLKKGHIISCGTSPSDVDFQVDFLKAH 241

Qy 243 QLGVPKITAFCKRLADRGV-SFKRLPI 268
Db 242 ELGVPKATHFADQLQKGTGVYTFEKLPI 268

RESULT 4
B69742
ABC transporter (ATP-binding protein) homolog ybaE - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
C/Accession: B69742
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hoisappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapido, A.; Lardinois,
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptratr, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:98044033; PMID:9384377
A/Accession: B69742
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-276 <KUN>
A/Cross-references: UNIPROT:P70970; GB:Z99104; GB:AL009126; NID:g2632267; PIDN:CAB11922.1
A/Experimental source: strain 168
C/Genetics:
A/Gene: ybaE
C/Superfamily: ATP-binding cassette homology
C/Keywords: ATP; nucleotide binding; P-loop
F:10-209/Domain: ATP-binding cassette homology <ABC>
F:27-34/Region: nucleotide-binding motif A (P-loop)

Query Match 52.6%; Score 729; DB 2; Length 276;
Best Local Similarity 56.4%; Pred. No. 2.1e-47;
Matches 146; Conservative 45; Mismatches 66; Indels 2; Gaps 2;

Qy 16 TPLASALSVDLSLTIEDGSGTALIGHTSGKSTILQLLGLLVPSQSVRVFDLTITSTS 75
Db 3 TPFERLALYDINASTKEGYSVAVTIGHTSGKSTILQLLGLLVPSQISLGVSTVIQAG 62

Qy 76 KKKDIQIRKQVGLVGFQFAENQIFETVLKDVAFGPNQFVSEEDAVKTAREKALVIGID 135
Db 63 KKKDLKKLKKVGVVFPQPEHQLFEETVLKDISFGPMNFGVKKEADEQKAREMLQLVGLS 122

Qy 136 ESLFDSPFELSGQMRRAIAGILAMEPAILVLDEPTAGLDPLGRKELMTLPKLLHQS 195
Db 123 BELLDSPFELSGQMRRAIAGILAMEPEVLVLDEPTAGLDPRGRKEIMDFELHQH 182

Qy 196 -MTVLVTHLMDVAVYANQVYVMEKGRVKGKPSDVDFQVFWMEVQLGVPKITAFCK 254
Db 193 NLTILVTHSHEDAAAYADEMIVMHKGTIQASGSPRDLFLKGEEMAGWGLDLPETIKFQR 242

Qy 255 RL-ADRGVSFKRLPIKIE 272
Db 243 HLEAALGVRFNEPLTIID 261

C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

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RESULT 5
AG1775
ABC transporter (ATP-binding protein) homolog lin2749 [imported] - Listeria innocua (str
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AG1775
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1775
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <GLA>
A:Cross-references: UNIPROT:Q8Y455; GB:AL592022; PIDN:CAC97975.1; PID:g16415285; GSPDB:G
A:Experimental source: strain Clip1262
C:Genetics:
A:Gene: lin2749
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
```

```
Query Match 50.2%; Score 696.5; DB 2; Length 288;
Best Local Similarity 50.6%; Pred. No. 6.2e-45;
Matches 137; Conservative 54; Mismatches 73; Indels 7; Gaps 2;
QY 1 MGIALENVFTYQEGTPLASALSDVSLTIEDGSGYALIGHTGSGKSTILOLNLGLLVP 60
DB 1 MEIKLEQLGQCYCKNSPFKRALLDVNSFDSGYSALIGHTGSGKSTILOLNLGLLMT 60
QY 61 QGSVRVFDLTITSTSKNDIQRKQVGLVFOFAENQIFETVLKDVAFQPNFGVSEED 120
DB 61 EKGITVGDREIVAGVKQKLDRLKRVGVFQPEAQLPEETVEKDICFGPMNFGVSEED 120
QY 121 AVKTAEREKALVGDIDSLFDRSPFELSGGQMRVAIAGILAMEPAIVLDELPTAGLDPLG 180
DB 121 AKLRKKVIYEVGLTEBILSRSPFELSGGQMRVAIAGVLAAMDPEVLVDELPTAGLDPHG 180
QY 181 RKELMTLFLKHL-QSGMTIVLTHLMDVVAEYANOVYVMEKRLVKGKPSDVFDQVWF 239
DB 181 REIMEMFYNLHKEGLTTLVTHSMEDAARYAEKIVLMKAGTVLQIGTFREIFAKPDEL 240
QY 240 EVQLGVPKITAFCKRLADRGVSFKRLPIKI 270
DB 241 VDLGLSPDVVRF-----QGLFERKFNVL 265
```

```
RESULT 6
AH1399
ABC transporter (ATP-binding protein) homolog lmo2600 [imported] - Listeria monocytogenes
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH1399
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1399
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <GLA>
A:Cross-references: UNIPROT:Q8Y455; GB:NC_003210; PIDN:CAD00678.1; PID:g16412088; GSPDB:
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo2600
```

```
Query Match 49.9%; Score 692.5; DB 2; Length 288;
Best Local Similarity 50.2%; Pred. No. 1.2e-44;
Matches 136; Conservative 55; Mismatches 73; Indels 7; Gaps 2;
QY 1 MGIALENVFTYQEGTPLASALSDVSLTIEDGSGYALIGHTGSGKSTILOLNLGLLVP 60
DB 1 MEIKLEQLGQCYCKNSPFKRALLDVNSFDSGYSALIGHTGSGKSTILOLNLGLLMT 60
QY 61 QGSVRVFDLTITSTSKNDIQRKQVGLVFOFAENQIFETVLKDVAFQPNFGVSEED 120
DB 61 EKGITVGDREIVAGVKQKLDRLKRVGVFQPEAQLPEETVEKDICFGPMNFGVSEED 120
QY 121 AVKTAEREKALVGDIDSLFDRSPFELSGGQMRVAIAGILAMEPAIVLDELPTAGLDPLG 180
DB 121 AKLRKKVIYEVGLTEBILSRSPFELSGGQMRVAIAGVLAAMDPEVLVDELPTAGLDPHG 180
QY 181 RKELMTLFLKHL-QSGMTIVLTHLMDVVAEYANOVYVMEKRLVKGKPSDVFDQVWF 239
DB 181 REIMEMFYNLHKEGLTTLVTHSMEDAARYAEKIVLMKAGTVLQIGTFREIFAKPDEL 240
QY 240 EVQLGVPKITAFCKRLADRGVSFKRLPIKI 270
DB 241 VDLGLSPDVVRF-----QGLFERKFNVL 265
```

```
RESULT 7
F97281
ABC-type transporter, ATPase component (cobalt transporters subfamily) CAC3101 [imported]
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: F97281
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: F97281
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <KUR>
A:Cross-references: UNIPROT:Q97EK9; GB:AE001437; PIDN:AAK81041.1; PID:g15026166; GSPDB:G
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC3101
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```
Query Match 49.2%; Score 683; DB 2; Length 286;
Best Local Similarity 47.7%; Pred. No. 6.3e-44;
Matches 133; Conservative 62; Mismatches 80; Indels 4; Gaps 3;
QY 1 MGIALENVFTYQEGTPLASALSDVSLTIEDGSGYALIGHTGSGKSTILOLNLGLLVP 60
DB 1 MPKIENLTYYTYPGTFPEKALDNNITIEDGEFAVFIGHTGSGKSTILOLNLGLLKP 60
QY 61 QGSVRVFDLTITSTSKNDIQRKQVGLVFOFAENQIFETVLKDVAFQPNFGVSEED 120
DB 61 SGSIFIDD--VDITDSKVLNDRKVKGLVFOYQPEVQLFEETIEKDIAGFRNWLSEEE 118
QY 121 AVKTAEREKALVGDIDSLF--DRSPFELSGGQMRVAIAGILAMEPAIVLDELPTAGLDPL 179
DB 119 VSTRVKKAMKMWGLEYNDFDKSPFELSGGQMRVAIAGVVAEMPKVLIIDPTAGLDPK 178
QY 180 GRKELMTLFLKHLQS-GMTIVLTHLMDVVAEYANOVYVMEKRLVKGKPSDVFDQVWF 238
DB 179 GRDDILYEIKKLQKEYNTIILVSHMEDVAKVADKIFVWYDSRCLISGNLDELVEFNIOT 238
QY 239 MEEVGLGVPKITAFCKRLADRGVSFKRLPIKIEEFKESL 277
DB 239 LEKVLAVPKVTYLVRLKREKGFIDSKDITIEAAKKEI 277
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RESULT 8

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E83670
ABC transporter (ATP-binding protein) BH0165 [imported] - Bacillus halodurans (strain C-
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 16-Aug-2004
C:Accession: E83670
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4333, 2000
A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: E83670
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-282 <STO>
A:Cross-references: UNIPROT:Q9KGD6; GB:BA000004; NID:g10172612; PIDN:BA8038
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0165
C:Superfamily: ATP-binding cassette homology

Query Match 46.0%; Score 637.5; DB 2; Length 282;
Best Local Similarity 52.6%; Pred. No. 1.6e-40;
Matches 130; Conservative 44; Mismatches 72; Indels 1; Gaps 1;

QY 14 EGTPLAALSVDSTIEDGSGYTLIGHTGSGKSTILOLLNGLLVPSQSGSVRPDLTITS 73
DB 2 KSGPPEKVALSDVSTIPSGSTAIIGHTGSGKSTLAQHFNGLLRPSKGTVRIGLELITA 61

QY 74 TSKNKDIRQIRKQVGLVFOFAENQIFFEETVLKDVAFQPNQFVSGVEDAVKAREKIALVG 133
DB 62 DQKPSLKEIRKVGVLVQYPEHQIFFEETVEKDICFGPMYGVSEARAKRKLHLVG 121

QY 134 IDESLFDRSPFELSGQGMRRVAIAGILAMEPAAILVLDSEPTAGLDPLGRKELMTLPKQLHQ 193
DB 122 LPDITYLQASPSLSGQGMRRVAIAGILAMEPDVLVLDSEPTAGLDPEGQRLIMDMFYRLHQ 181

QY 194 -SGMTIVLVTHLMDVDAEVANQVYVMEKRLVKGKPSDVFODVVFMEEVQVGPKITAF 252
DB 182 EKELTVLVTHNMSDAAKPADQIIIVSQGNVAMTGDRTQVFARADELVAGLDVDPETLQL 241

QY 253 CKRLADR 259
DB 242 LIQVKER 248

RESULT 9
C90560
ABC transporter atp-binding protein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 16-Aug-2004
C:Accession: C90560
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A>Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A95512; MUID:21267165; PMID:11353084
A:Accession: C90560
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-304 <KUR>
A:Cross-references: UNIPROT:Q98QH4; GB:AL445566; PID:g14089801; PIDN:CAC13560.1; GSPDB:G
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPU_3870
A:Genetic code: SGC3
C:Superfamily: ATP-binding cassette homology

Query Match 42.9%; Score 595.5; DB 2; Length 304;
Best Local Similarity 41.4%; Pred. No. 2.5e-37;
Matches 122; Conservative 66; Mismatches 88; Indels 19; Gaps 5;

QY 1 MGIALENVNTFYQEGTPLAALSVDLSLTIEDGSGYTLIGHTGSGKSTILOLLNGLLVPS 60
DB 1 MGIIVKNISYIYNKNTALKALDSDSCINQGEHVAIIIGTSGKTFIEHNLALLIPE 60
```

```
61 QGSVR-VP-----DTLITST--SKNKDIRQIRKQVGLVFOFAENQIFFEETVL 104
DB 61 TGTINWIFENSHKTKKYLEVDVVLKRTYFKVKVAKDIRRIGVVFQFAEQYFEEETIE 120

QY 105 KDVAFGPQNFVSGVEDAVKAREKIALVGDIDSLFDRSPFELSGQGMRRVAIAGILAMEP 164
DB 121 KDINFGPRSYGVSEKAKQRAAKVLEWVGLPLEPLEKNPFGLSGQGMRRVAIAGILAE 180

QY 165 AILVLDSEPTAGLDPLGRKELMTLPKQLHQSGMTIVLVTHLMDVDAEVANQVYVMEKRLV 224
DB 181 DPLVLDSEPTAGLDPLGRKELMTLPKQLHQSGMTIVLVTHLMDVDAEVANQVYVMEKRLV 240

QY 225 KGGKPSDVFODVVFMEEVQVGPKITAFCKELADRGVSFKELPI-KIEEFKESLN 278
DB 241 RDAQTYEILKDEKFLVKNLSPKLIITFVNKLEORGIFLK--PVTSIDKLAIELN 293

RESULT 10
H90018
hypochemical protein SA2020 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 16-Aug-2004
C:Accession: H90018
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci
ma, A.; Mizutani-Ts, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90018
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <KUR>
A:Cross-references: UNIPROT:Q99S48; GB:BA000018; PID:g13702021; PIDN:BA843313.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA2020
C:Superfamily: ATP-binding cassette homology

Query Match 42.5%; Score 589.5; DB 2; Length 286;
Best Local Similarity 44.8%; Pred. No. 6.5e-37;
Matches 112; Conservative 61; Mismatches 76; Indels 1; Gaps 1;

QY 1 MGIALENVNTFYQSGTPLAALSVDLSLTIEDGSGYTLIGHTGSGKSTILOLLNGLLVPS 60
DB 1 MTRIPDNVSYTYQKGTPTQHOAIDHVNTEPESQGYAIVGQTGSGKSTLIQINALLKPT 60

QY 61 QGSVRVPDLTITSTSKNKDIRQIRKQVGLVFOFAENQIFFEETVLKDVAFQPNQFVSGVED 120
DB 61 TGTVTVDITITHKTKKYLIPVPRKRIQWVQFPESQLFEDTVREMIFGPNFKNWILDE 120

QY 121 AVKTAREKIALVGDIDSLFDRSPFELSGQGMRRVAIAGILAMEPAAILVLDSEPTAGLDPLG 180
DB 121 AKNYAHLRLMDLGFSDRVMSQSPFGSGQGMRRVAIAGILAMEPAAILVLDSEPTAGLDPLG 180

QY 181 RKELMTLPKQLH-QSGMTIVLVTHLMDVDAEVANQVYVMEKRLVKGKPSDVFODVVFPM 239
DB 181 KRQVNRLLKSLQTDENKAILIISHDMNEVARYADEIVVMKESIVSQTSFKELPKDKKCL 240

QY 240 EEVQLGVPKI 249
DB 241 ADWHIGLPEI 250

RESULT 11
I64219
membrane transport protein (glnQ) homolog MG180 - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 16-Aug-2004
C:Accession: I64219
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.N.
, C.A.; Venter, J.C.
```

Science 270, 397-403, 1995
A>Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: I64219
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-304 <TIGR>
A;Cross-references: UNIPROT:P47426; GB:U39695; GB:L43967; NID:g1045864; TIGR:1045864; MIM:1045864
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3
A;Start codon: GTG
C;Superfamily: ATP-binding cassette homology
C;Keywords: ATP; nucleotide binding; P-loop
F;37-236/Domain: ATP-binding cassette homology <ABC>
F;54-61/Region: nucleotide-binding motif A (P-loop)

Query Match 39.0%; Score 540.5; DB 2; Length 304;
Best Local Similarity 40.2%; Pred. No. 3.3e-33;
Matches 113; Conservative 55; Mismatches 108; Indels 5; Gaps 2;

QY 3 IALENNFTYQEGTPLASALSDVSLTIEDGVTALIGHTSGKSTILQLLNGLLVPSSQ 62
DB 17 LAVSHLSVFNSTNNPIKVIDFSYTFQKQNIYCIIGDSGSGKSTLVNHFNGLIKPNQ 76

QY 63 SVRVFTLLI-TSTSKNKDRIQIRKQVGLVFOFAENQIFETVLKDVAFQPNFGVSEDA 121
DB 77 DIWVKDIYIGAKQKIKNFKKLAKTISIVFPFQYQLFKDVTVEKDMFGFVALGQSKYDA 136

QY 122 VKTAREKALVIGIDESLFDSPFELSGQRRVAIAGILAMEPAIILVDEPTAGLDPLGR 181
DB 137 RQKAAAYLEMGKLVYFLEKPNFELSGQRRVAIAGILAMEPAIILVDEPTAGLDPEGE 196

QY 182 KELMTLFFKLLHOSGMTIVLVTHLMDVVAENQVYVMEKGRVKGKSPDVFODVVFME 241
DB 197 REMWQLIKTAKQKQRTVFMITHQMNVLVADVLVLAQKLVKAAAPYEVFMDQTFLEK 256

QY 242 VOLGVPKITAFCKRLADRGVSKRL-----PIKIEEPKESLN 278
DB 257 TTIVPPVIQVVKDLINAHFNKLELQPNLEQLASAIN 297

RESULT 12
S62814
histidine transport ATP-binding protein hisP - Mycoplasma pneumoniae (strain ATCC 29342)
N;Alternate names: glutamine transport protein GlnQ homolog; hypothetical protein G9_04
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 16-Aug-2004
R;Hilbert, H.; Himmelfreid, R.; Plagens, H.; Herrmann, R.
Nucleic Acids Res. 24, 628-639, 1996
A;Title: Sequence analysis of 56 kb from the genome of the bacterium Mycoplasma pneumoniae
A;Reference number: S62797; MUID:96177562; PMID:8604303
A;Accession: S62814
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-303 <HIL>
A;Cross-references: UNIPROT:Q50293; EMBL:U34795; NID:g1215683; PIDN:AAC3687.1; PID:g121
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
R;Himmelfreid, R.; Hilbert, H.; Plagens, H.; Pirkil, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A;Reference number: S73327; MUID:97105885; PMID:8948633
A;Accession: S73963
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-303 <HIM>
A;Cross-references: EMBL:AE000061; GB:U00089; NID:g1674336; PIDN:AAB96285.1; PID:g167434
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C;Genetics:
A;Gene: hisP
A;Genetic code: SGC3

C;Superfamily: ATP-binding cassette homology
C;Keywords: ATP; nucleotide binding; P-loop
F;37-236/Domain: ATP-binding cassette homology <ABC>
F;54-61/Region: nucleotide-binding motif A (P-loop)

Query Match 38.5%; Score 533.5; DB 2; Length 303;
Best Local Similarity 39.5%; Pred. No. 1.1e-32;
Matches 111; Conservative 58; Mismatches 107; Indels 5; Gaps 2;

QY 3 IALENNFTYQEGTPLASALSDVSLTIEDGVTALIGHTSGKSTILQLLNGLLVPSSQ 62
DB 17 LSVNLSVCFNEKTVHEVKNVDNFSTYTFANKVYCIIGDSGSGKSTLVNHFNGLIKPNQ 76

QY 63 SVRVFTLLI-TSTSKNKDRIQIRKQVGLVFOFAENQIFETVLKDVAFQPNFGVSEDA 121
DB 77 DIWVKDIYIGAKQKIKNFKKLAKTISIVFPFQYQLFKDVTVEKDMFGFVALGQSKNEA 136

QY 122 VKTAREKALVIGIDESLFDSPFELSGQRRVAIAGILAMEPAIILVDEPTAGLDPLGR 181
DB 137 RQKAAAYLEMGKLVYFLEKPNFELSGQRRVAIAGILAMEPAIILVDEPTAGLDPEGE 196

QY 182 KELMTLFFKLLHOSGMTIVLVTHLMDVVAENQVYVMEKGRVKGKSPDVFODVVFME 241
DB 197 REMWQLIKTAKQKQRTVFMITHQMNVLVADVLVLAQKLVKAAAPYEVFMDQTFLEK 256

QY 242 VOLGVPKITAFCKRLADRGVSKRL-----PIKIEEPKESLN 278
DB 257 TTIVPPVIQVVKDLINAHFNKLELQPNLEQLASAIN 297

RESULT 13
G64435
cobalt transport ATP-binding protein O homolog - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
A;Accession: G64435
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.;
rsen, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: G64435
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-279 <BUL>
A;Cross-references: UNIPROT:Q58488; GB:U67551; GB:L77117; NID:g1591728; PIDN:AAB99089.1;
C;Genetics:
A;Map position: REV1027976-1027137
C;Superfamily: ATP-binding cassette homology
C;Keywords: ATP; nucleotide binding; P-loop
F;37-215/Domain: ATP-binding cassette homology <ABC>
F;37-44/Region: nucleotide-binding motif A (P-loop)

Query Match 36.9%; Score 511.5; DB 2; Length 279;
Best Local Similarity 42.1%; Pred. No. 4.4e-31;
Matches 107; Conservative 53; Mismatches 73; Indels 21; Gaps 4;

QY 3 IALENNFTYQEGTPLASALSDVSLTIEDGVTALIGHTSGKSTILQLLNGLLVPSSQ 62
DB 4 VETKOLYFRYPDGT-----AVLKGINKVKKGVVSLGPNAGAGKSTLFLHFNGLRPTKG 59

QY 63 SVRVFTLLTSTSKNKDRI-----QIRKQVGLVFOFAENQIFETVLKDVAFQPNFG 115
DB 60 EVLI-----KGRPKIKYDKSLVEVRKTVGLVFNQPDQIFAPTVADVAPGPNLNG 110

QY 116 VSEDAVKTAREKALVIGIDESLFDSPFELSGQRRVAIAGILAMEPAIILVDEPTAG 175
DB 111 LPKEEVEKRVKEALKAVGM-EGENKPPHLSGQKRVVAIAGILAMEPAIILVDEPTAG 169

QY 176 LDPLGRKELMTLFFKLLHOSGMTIVLVTHLMDVVAENQVYVMEKGRVKGKSPDVFOD 235

